

FIG. 1A

1 agggagaggc agtgaccatg aaggctgtgc tgcttgccct gttgatggca
51 ggcttgcccc tgcagccagg cactgccctg ctgtgctact cctgcaaagc
101 ccaggtgagc aacgaggact gcctgcaggt ggagaactgc acccagctgg
151 gggagcagtg ctggaccgcg cgcacccgcg cagttggcct cctgaccgtc
201 atcagcaaag gctgcagctt gaactgcgtg gatgactcac aggactacta
251 cgtgggcaag aagaacatca cgtgctgtga caccgacttg tgcaacgcca
301 gcggggccca tgccctgcag ccggctgccc ccacccctgc gctgctccct
351 gcactcggcc tgctgctctg gggacccggc cagctatagg ctctgggggg
401 ccccgctgca gcccacactg ggtgtggtgc cccaggcctt tgtgccactc
451 ctcacagaac ctggcccagt gggagcctgt cctgggttcct gaggcacatc
501 ctaacgcaag tttgaccatg tatgtttgca ccccttttcc ccnaaccctg
551 accttcccat gggccttttc caggattccn accnggcaga tcagtttttag
601 tganacanat ccgcntgcag atggcccctc caacnnttn tgtgntggt
651 tccatggccc agcatttttc acccttaacc ctgtgttcag gcacttnttc
701 cccaggaag cttccctgc ccacccatt tatgaattga gccagggttg
751 gtccgtggtg tccccgcac ccagcagggg acaggcaatc aggagggccc
801 agtaaaggct gagatgaagt ggactgagta gaactggagg acaagagttg
851 acgtgagttc ctgggagttt ccagagatgg ggcctggagg cctggaggaa
901 ggggccaggc ctcacatttg tgggntccc gaatggcagc ctgagcacag
951 cgtaggccct taataaacac ctgttgata agccaaaaaa aaaaaaaa

FIG. 1B

MKAVLLALLMAGLALQPGTALLCYSCAQVSNECLQV
ENCTQLGEQCWTARIRAVGLLTVISKGCSLNCVDDS
QDYVVGKKNITCCDLDLCNASGAHALQPAAAILALLPAL
GLLLWGPQQL

FIG. 2

1 ATGAAGACAGTTTTTTTTATCCTGCTGGCCACCTACTTAGCCCTGCATCCAGGTGCTGCT
 -----+-----+-----+-----+-----+-----+ 60
 TACTTCTGTCAAAAAAATAGGACGACCGGTGGATGAATCGGGACGTAGGTCCACGACGA

 M K T V F F I L L A T Y L A L H P G A A

 CTGCAGTGCTATTCATGCACAGCACAGATGAACAACAGAGACTGTCTGAATGTACAGAAC
 61 -----+-----+-----+-----+-----+-----+ 120
 GACGTCACGATAAGTACGTGTCGTGTCTACTTGTTGTCTCTGACAGACTTACATGTCTTG

 L Q C Y S C T A Q M N N R D C L N V Q N

 TGCAGCCTGGACCAGCACAGTTGCTTTACATCGCGCATCCGGGCCATTGGACTCGTGACA
 121 -----+-----+-----+-----+-----+-----+ 180
 ACGTCGGACCTGGTCGTGTCAACGAAATGTAGCGCGTAGGCCCGGTAACCTGAGCACTGT

 C S L D Q H S C F T S R I R A I G L V T

 GTTATCAGTAAGGGCTGCAGCTCACAGTGTGAGGATGACTCGGAGAACTACTATTTGGGC
 181 -----+-----+-----+-----+-----+-----+ 240
 CAATAGTCATTCCCAGCGTCGAGTGTCACTCTACTGAGCCTCTTGATGATAAACCCG

 V I S K G C S S Q C E D D S E N Y Y L G

 AAGAAGAACATCACGTGCTGCTACTCTGACCTGTGCAATGTCAACGGGGCCCACACCCTG
 241 -----+-----+-----+-----+-----+-----+ 300
 TTCTTCTTGTAGTGACGACGATGAGACTGGACACGTTACAGTTGCCCCGGGTGTGGGAC

 K K N I T C C Y S D L C N V N G A H T L

 AAGCCACCCACCACCCTGGGGCTGCTGACCGTGCTCTGCAGCCTGTTGCTGTGGGGCTCC
 301 -----+-----+-----+-----+-----+-----+ 360
 TTCGGTGGGTGGTGGGACCCGACGACTGGCACGAGACGTCGGACAACGACACCCCGAGG

 K P P T T L G L L T V L C S L L L W G S

 AGCCGTCTGTAGGCTCTGGGAGAGCCTACCATAGCCCGATTGTGAAGGGATGAGCTGCAC
 361 -----+-----+-----+-----+-----+-----+ 420
 TCGGCAGACATCCGAGACCCTCTCGGATGGTATCGGGCTAACACTTCCTACTCGACGTG

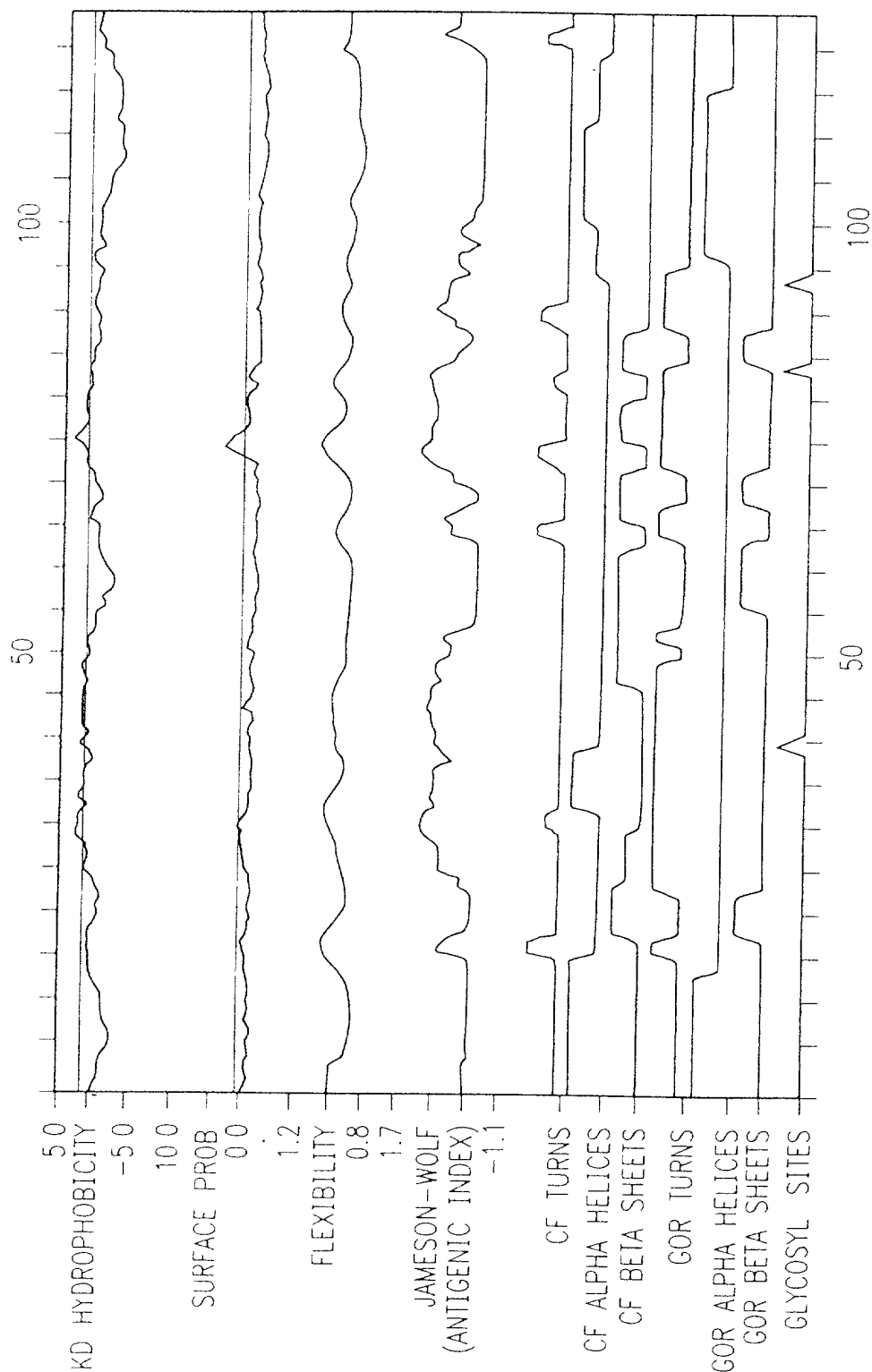
 S R L *

 TCCACCCACCCACACAGG
 421 -----+-----+-----+ 441
 AGGTGGGGTGGGGGTGTGTCC

	1980	1981	1982	1983	1984	1985	1986	1987	1988	1989	1990	1991	1992	1993	1994	1995	1996	1997	1998	1999	2000	2001	2002	2003	2004	2005	2006	2007	2008	2009	2010	2011	2012	2013	2014	2015	2016	2017	2018	2019	2020	2021	2022	2023	2024	2025	2026	2027	2028	2029	2030	2031	2032	2033	2034	2035	2036	2037	2038	2039	2040	2041	2042	2043	2044	2045	2046	2047	2048	2049	2050	2051	2052	2053	2054	2055	2056	2057	2058	2059	2060	2061	2062	2063	2064	2065	2066	2067	2068	2069	2070	2071	2072	2073	2074	2075	2076	2077	2078	2079	2080	2081	2082	2083	2084	2085	2086	2087	2088	2089	2090	2091	2092	2093	2094	2095	2096	2097	2098	2099	2100
1980	1981	1982	1983	1984	1985	1986	1987	1988	1989	1990	1991	1992	1993	1994	1995	1996	1997	1998	1999	2000	2001	2002	2003	2004	2005	2006	2007	2008	2009	2010	2011	2012	2013	2014	2015	2016	2017	2018	2019	2020	2021	2022	2023	2024	2025	2026	2027	2028	2029	2030	2031	2032	2033	2034	2035	2036	2037	2038	2039	2040	2041	2042	2043	2044	2045	2046	2047	2048	2049	2050	2051	2052	2053	2054	2055	2056	2057	2058	2059	2060	2061	2062	2063	2064	2065	2066	2067	2068	2069	2070	2071	2072	2073	2074	2075	2076	2077	2078	2079	2080	2081	2082	2083	2084	2085	2086	2087	2088	2089	2090	2091	2092	2093	2094	2095	2096	2097	2098	2099	2100	

[illegible]

FIG. 4



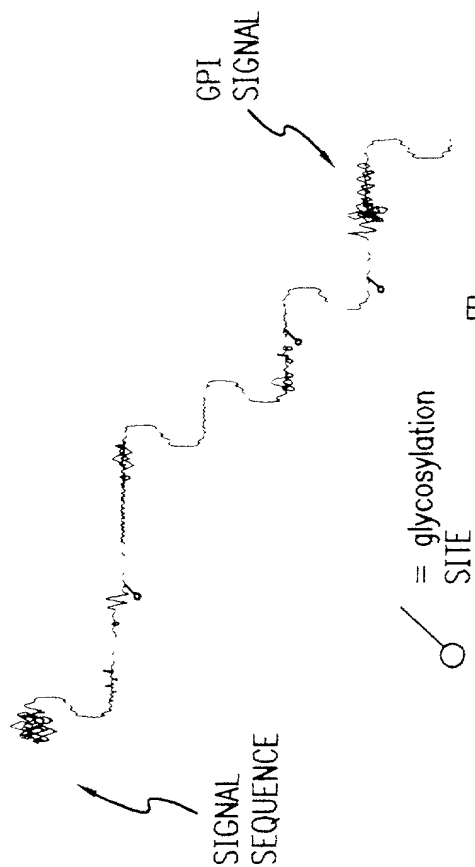


FIG. 5

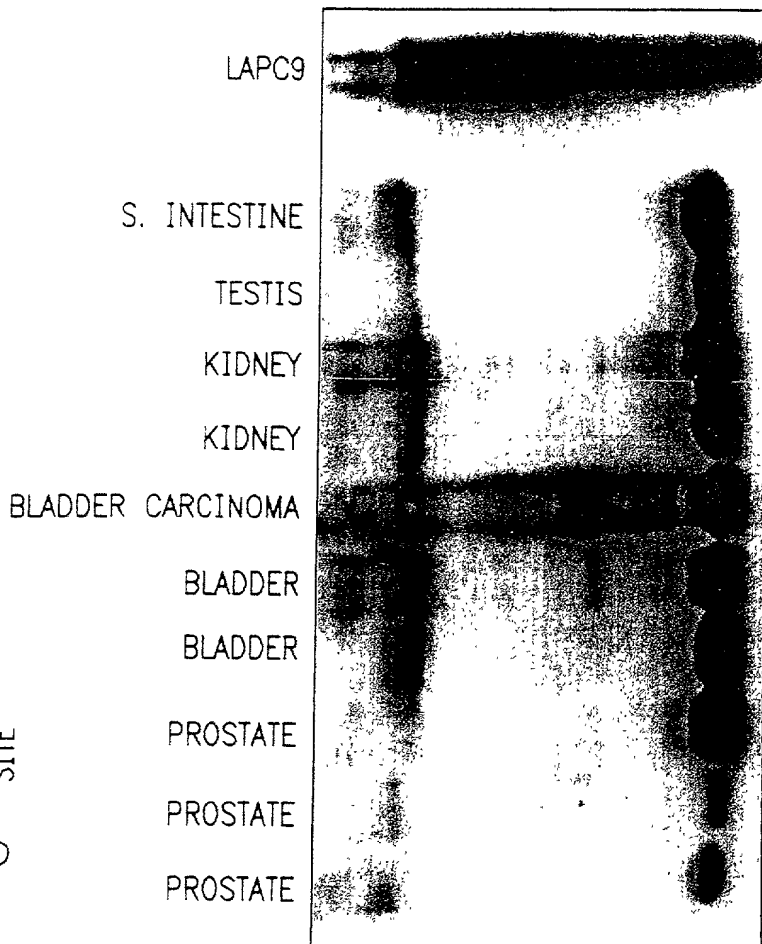


FIG. 6

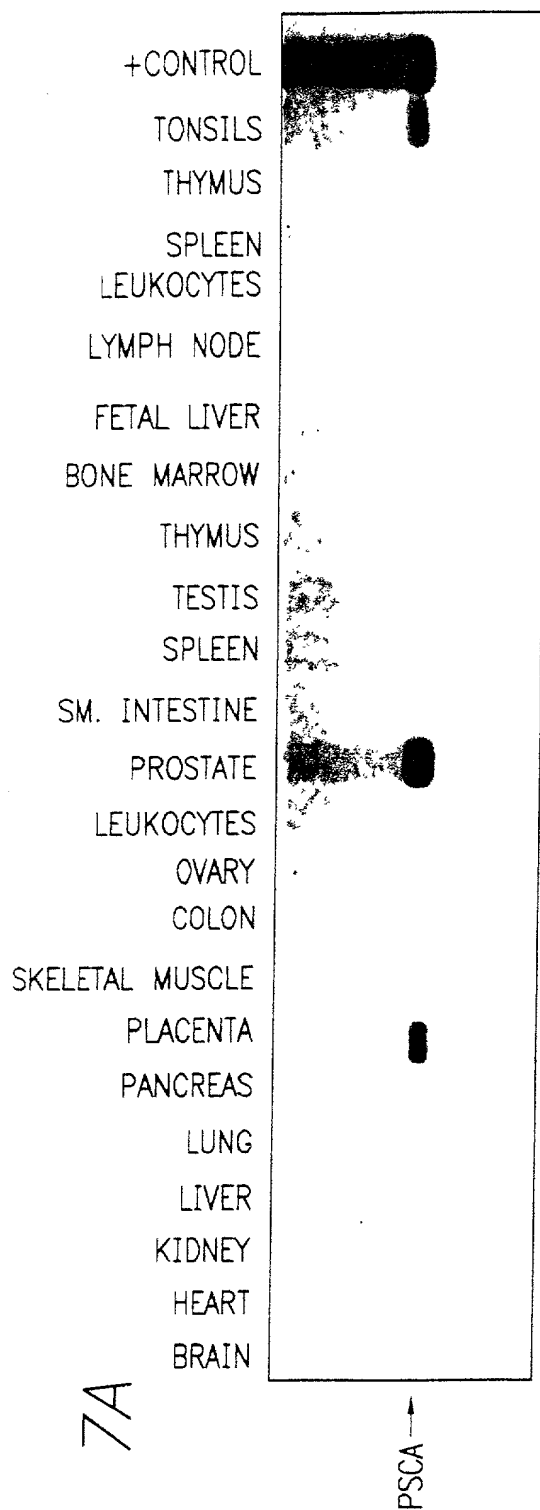


FIG. 7A

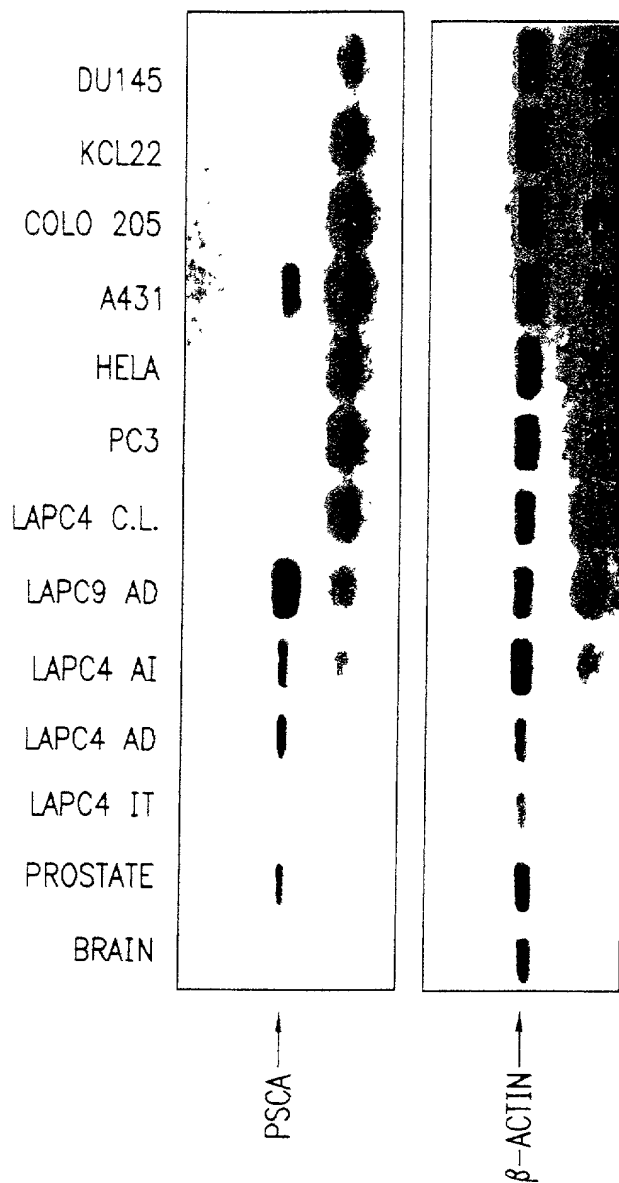


FIG. 7B

FIG. 8A

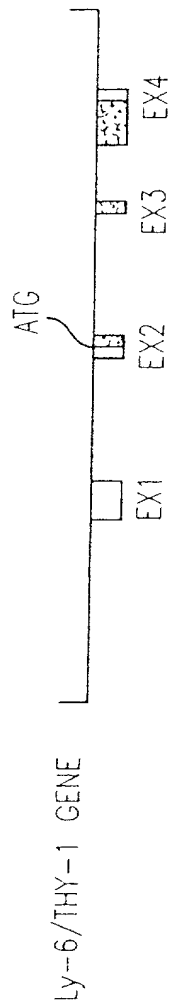


FIG. 8B

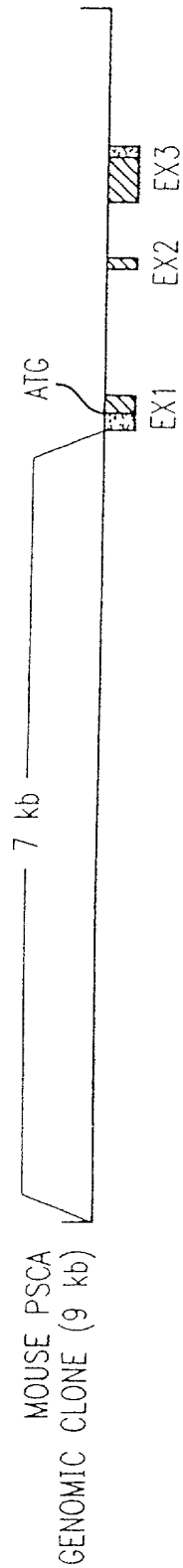


FIG. 8C

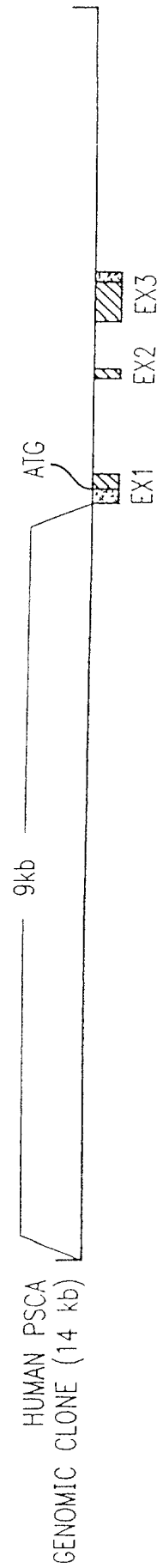


FIG. 9A

103620 6345360

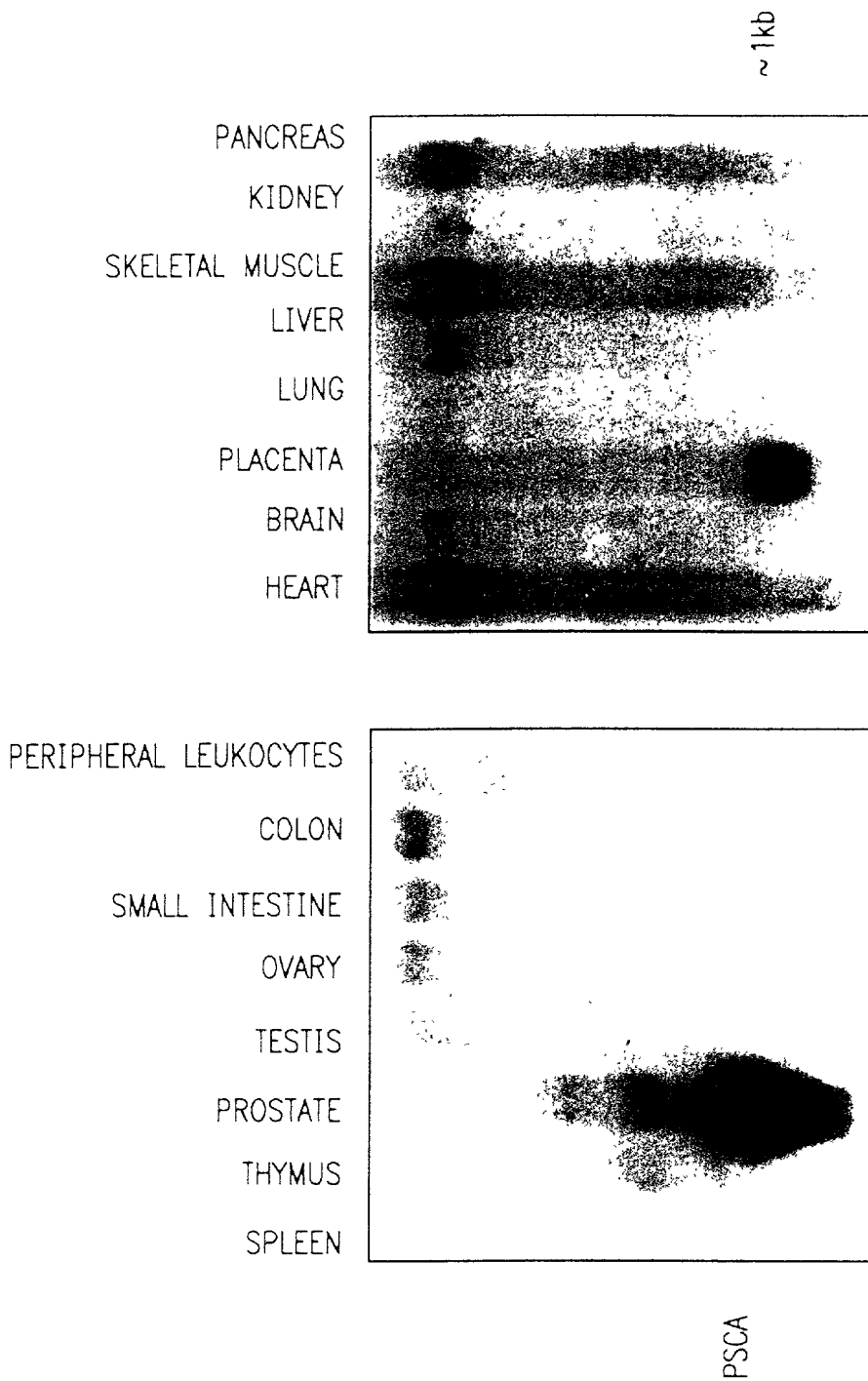


FIG. 9B

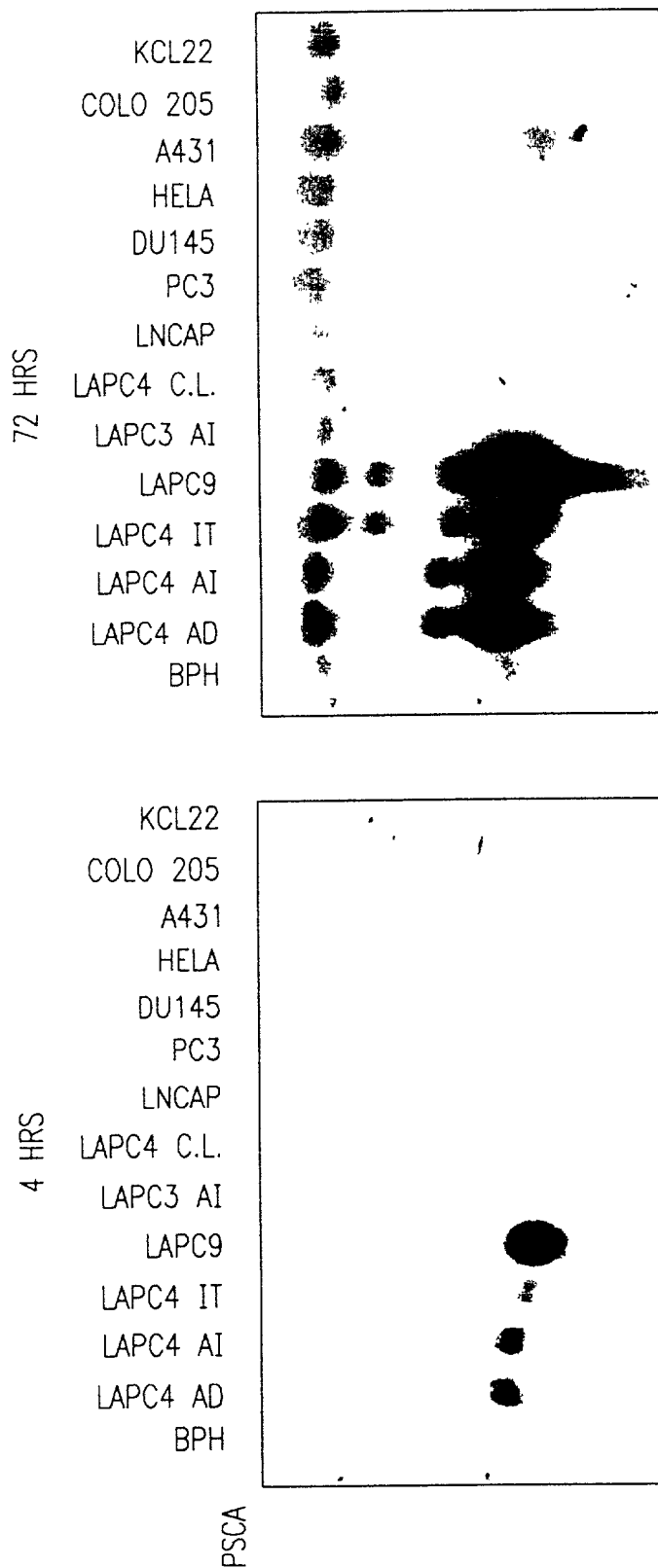


FIG. 10A

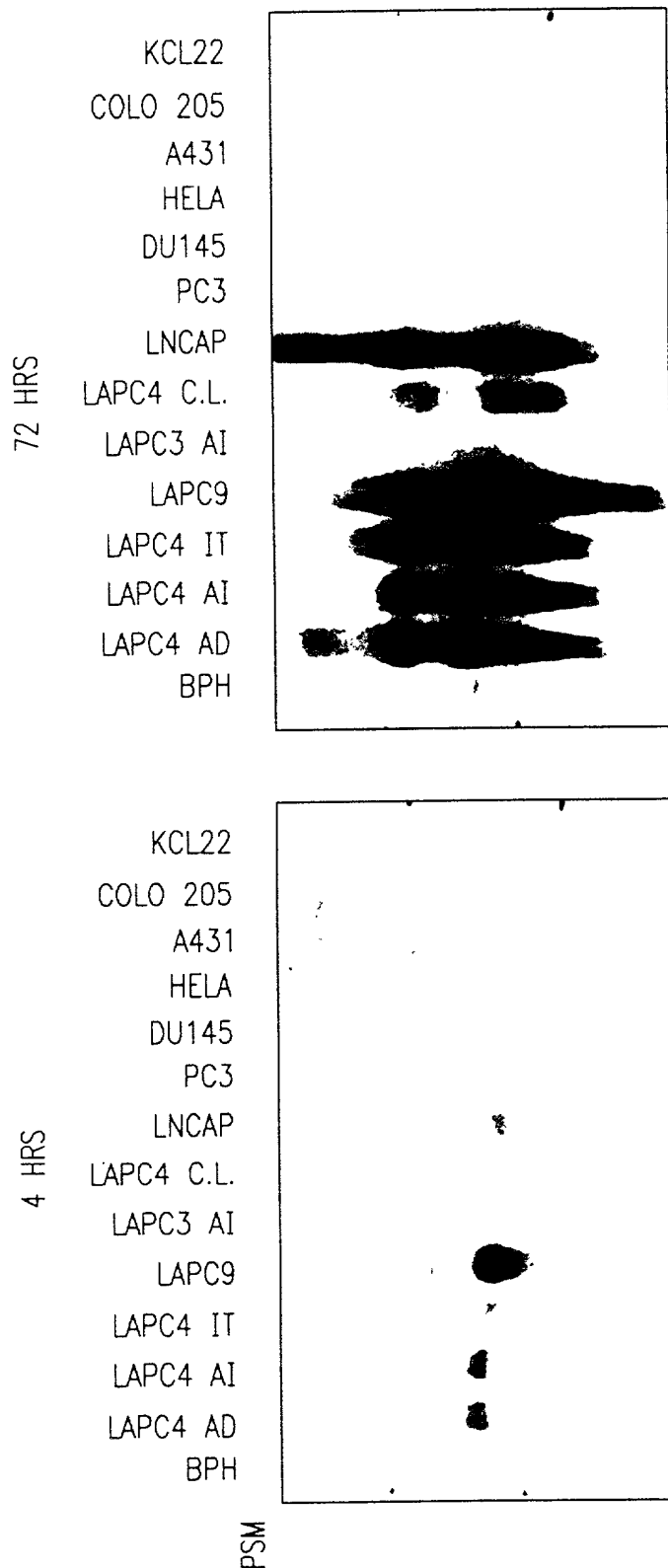
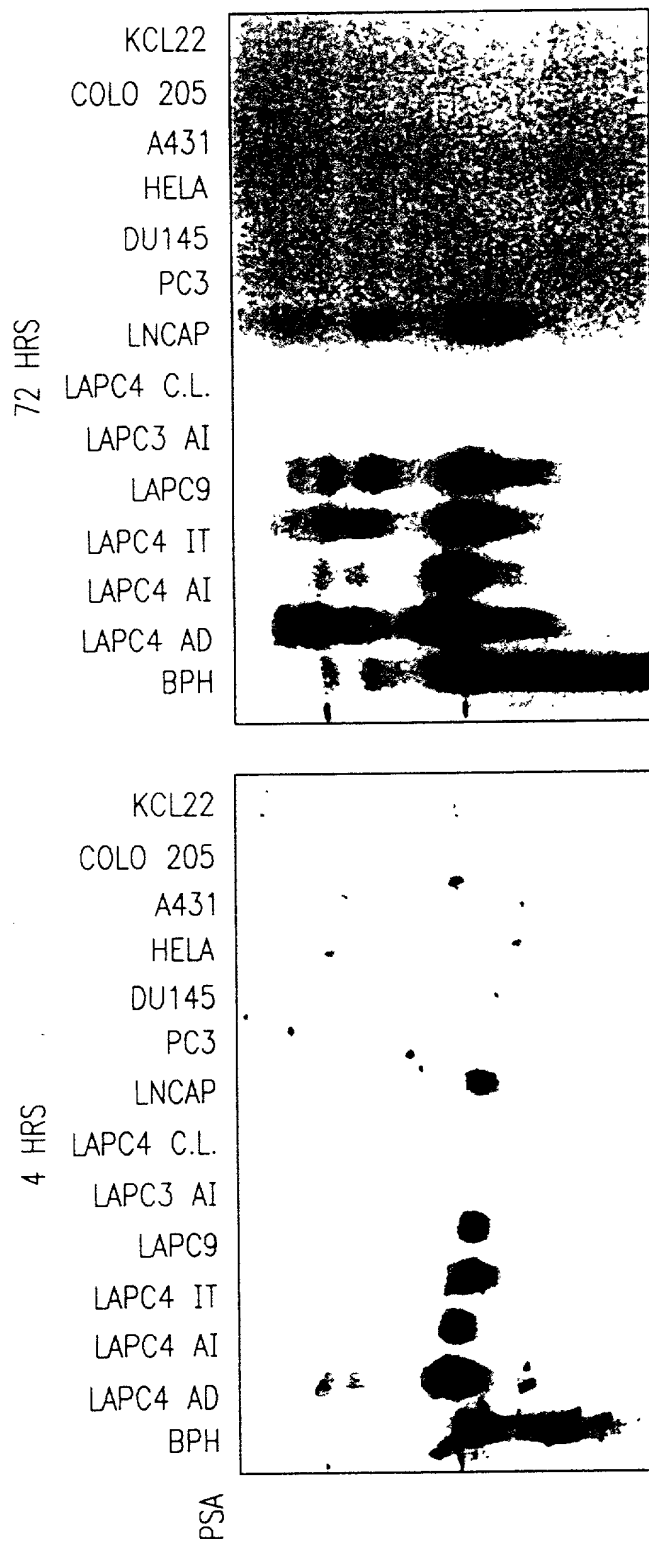


FIG. 10B



ETBR

FIG. 10C

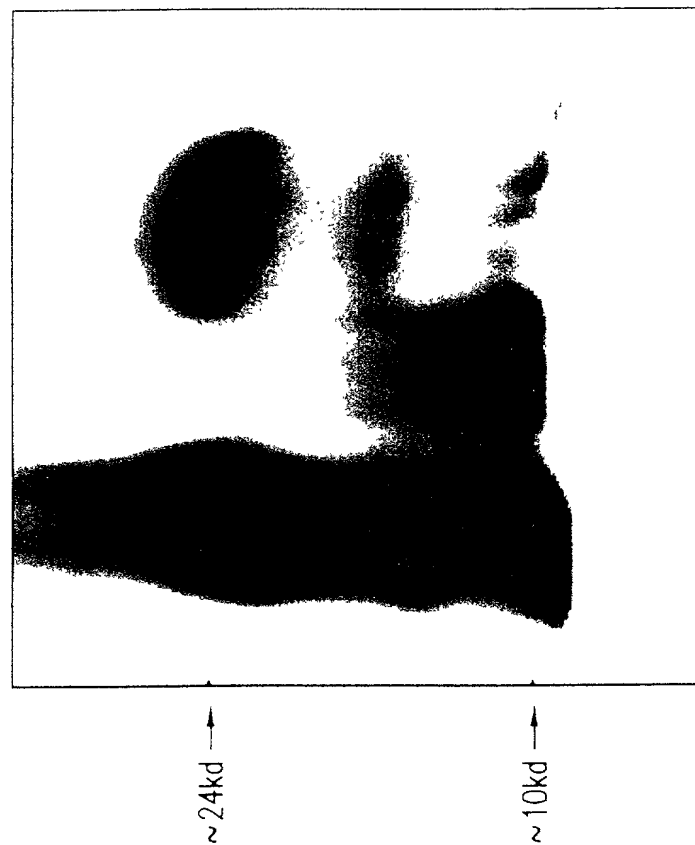


FIG. 11C

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FIG. 12A

CONTROL
N GLYCOSIDASE F
O GLYCOSIDASE



CELL ASSOCIATED
SECRETED

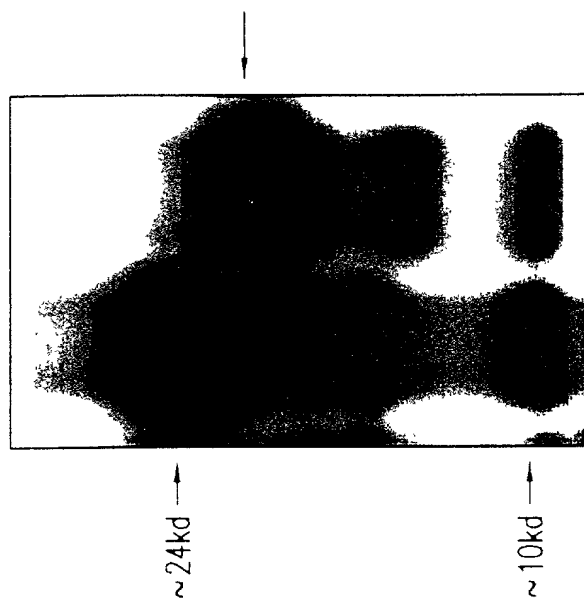


FIG. 12B

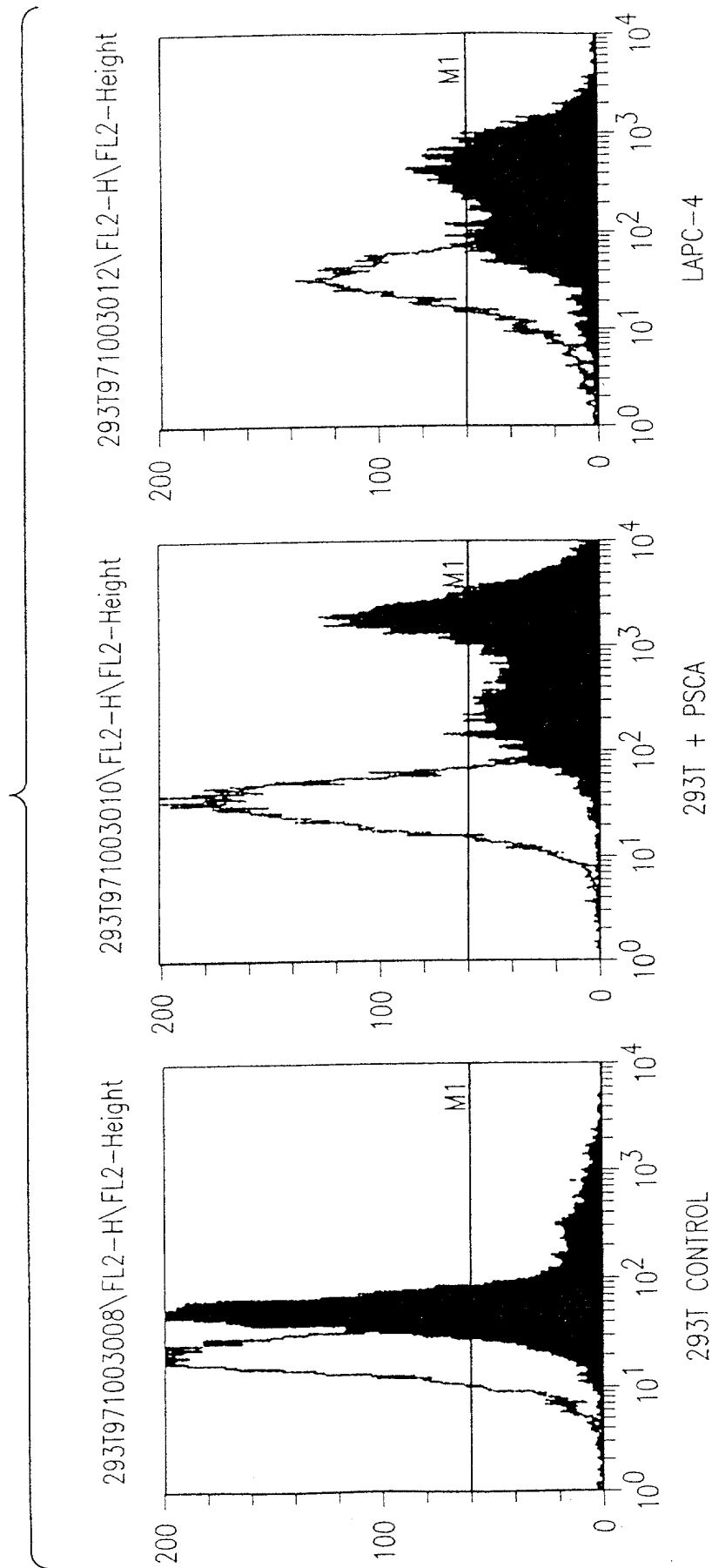
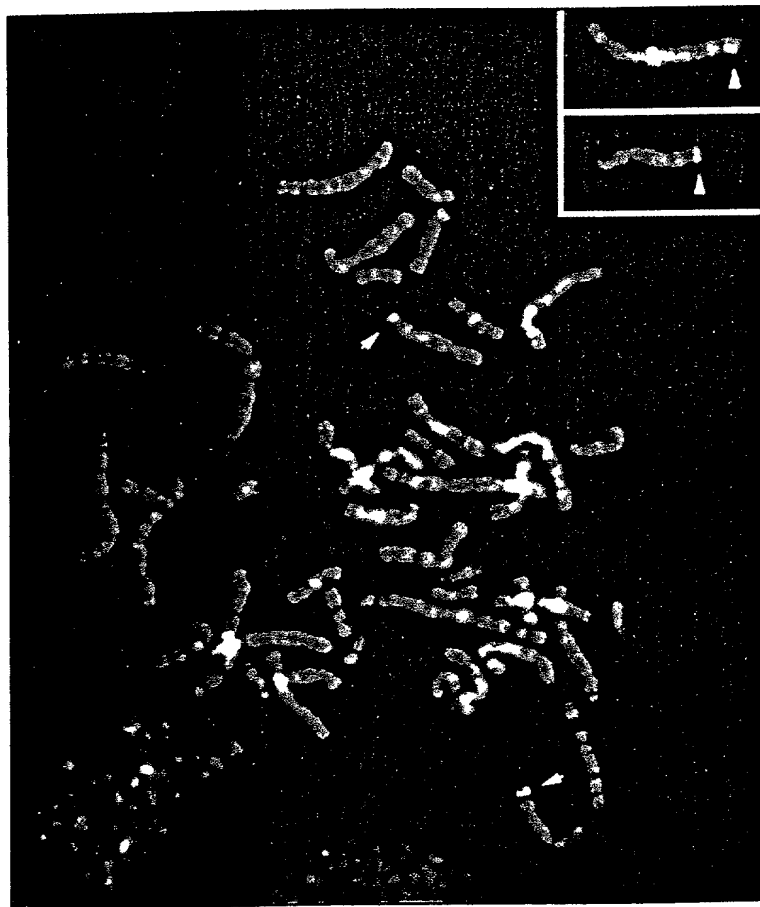


FIG. 12C

FIG. 13



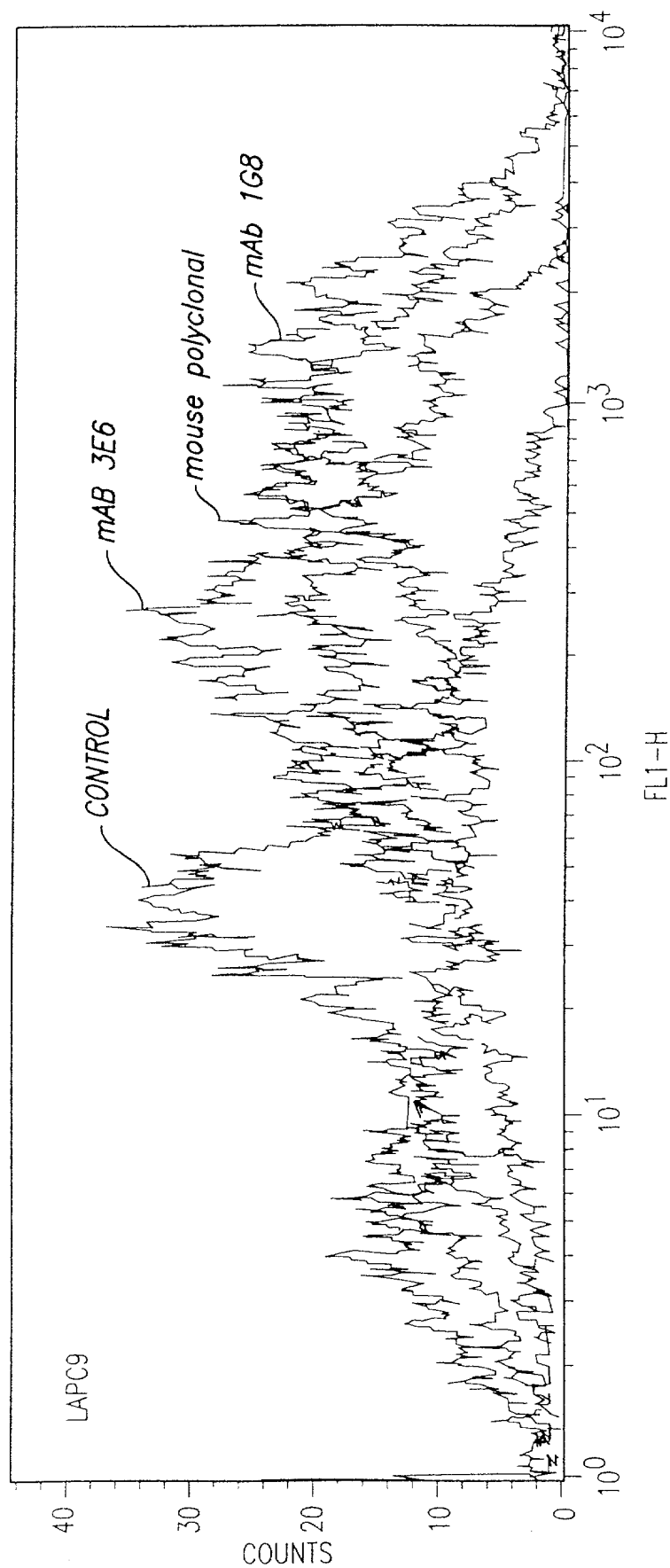


FIG. 14B

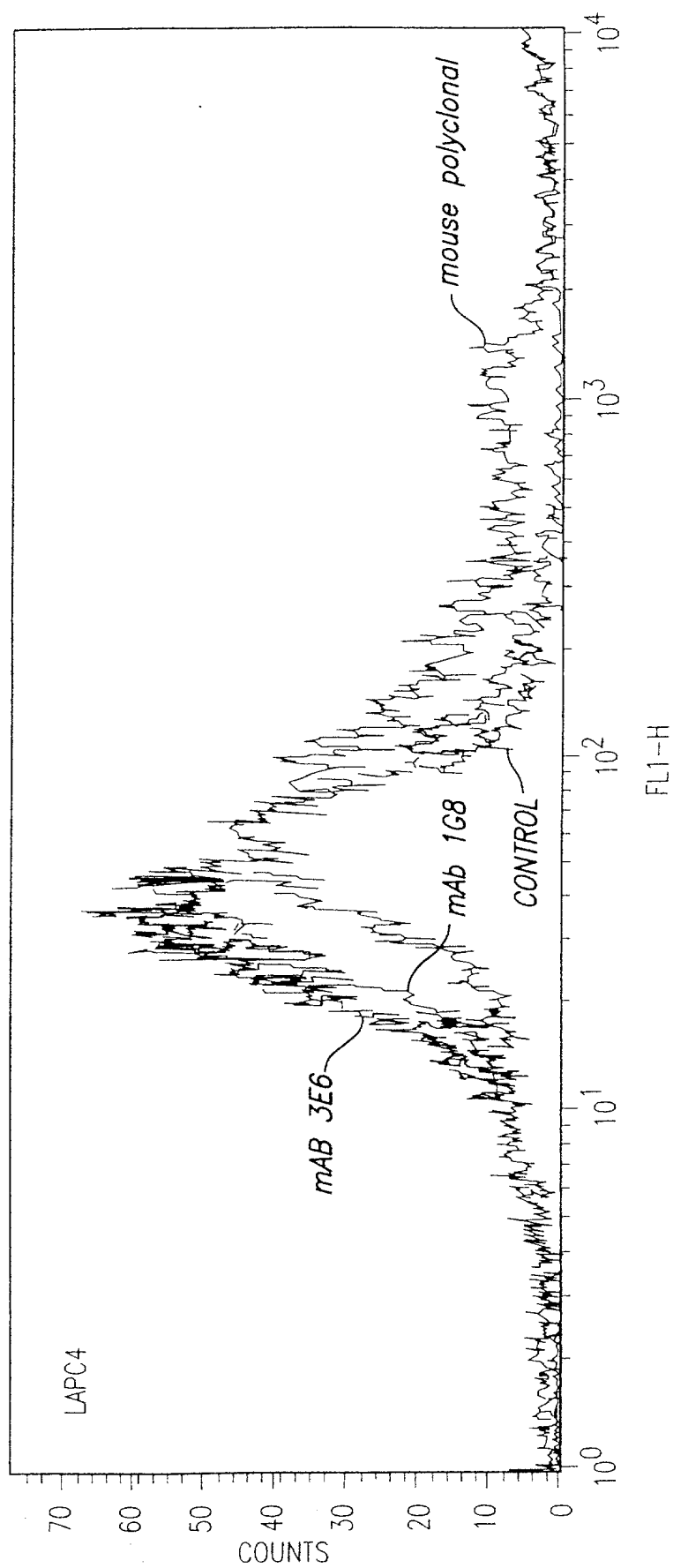
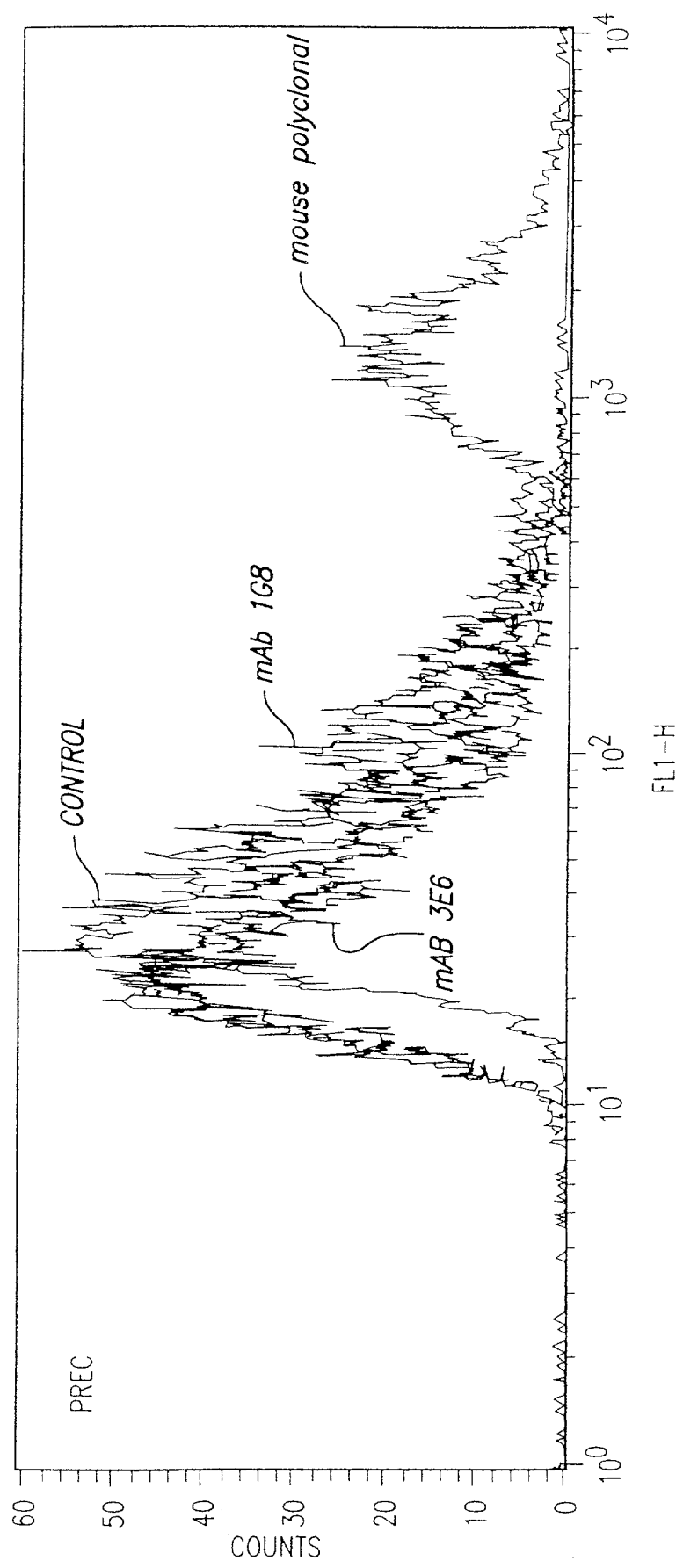


FIG. 14C



PROSTATE STEM CELL ANTIGEN (PSCA) IS A GPI-ANCHORED PROTEIN

1	M	K	I	F	P	V	L	L	A	A	L	L	G	V	E	R	A	S	hSCA-2
11	M	K	A	V	L	L	A	L	L	M	A	G	L	A	L	Q	P	G	hPSCA
11	M	K	T	V	L	F	L	L	A	T	Y	L	A	L	H	P	C	A	mPSCA
21	L	M	C	F	S	C	L	N	Q	K	S	N	L	Y	C	L	K	P	T
21	L	C	Y	S	C	K	A	Q	V	S	N	E	D	C	L	Q	V	E	N
21	L	Q	C	Y	S	C	T	A	Q	M	N	N	R	D	C	L	N	V	N
41	C	S	D	Q	D	N	Y	C	V	T	V	S	A	S	A	G	I	G	N
41	C	T	Q	L	G	E	Q	C	W	T	A	R	I	R	A	V	C	L	L
41	C	S	L	D	Q	H	S	C	F	I	S	R	I	R	A	I	C	L	V
61	V	T	F	G	H	S	L	S	K	T	C	S	P	A	C	P	I	P	E
61	V	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	
61	V	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	
81	V	N	V	G	V	A	S	M	G	I	S	C	C	Q	S	F	E	C	N
76	D	Y	Y	V	C	R	K	-	-	-	-	-	-	-	-	-	-	-	-
76	N	Y	Y	L	C	K	K	-	-	-	-	-	-	-	-	-	-	-	-
101	S	A	A	D	G	G	L	R	A	S	V	T	L	L	G	A	G	L	L
95	S	G	A	H	A	L	Q	P	A	A	A	I	L	A	L	P	A	L	G
95	N	C	A	H	T	L	K	P	P	T	T	L	G	L	L	T	V	L	C
121	S	L	L	P	A	L	L	R	F	G	P	-	-	-	-	-	-	-	-
115	L	L	L	W	C	P	G	Q	L	-	-	-	-	-	-	-	-	-	-
115	L	L	L	W	C	S	S	R	L	-	-	-	-	-	-	-	-	-	-

FIG. 16A

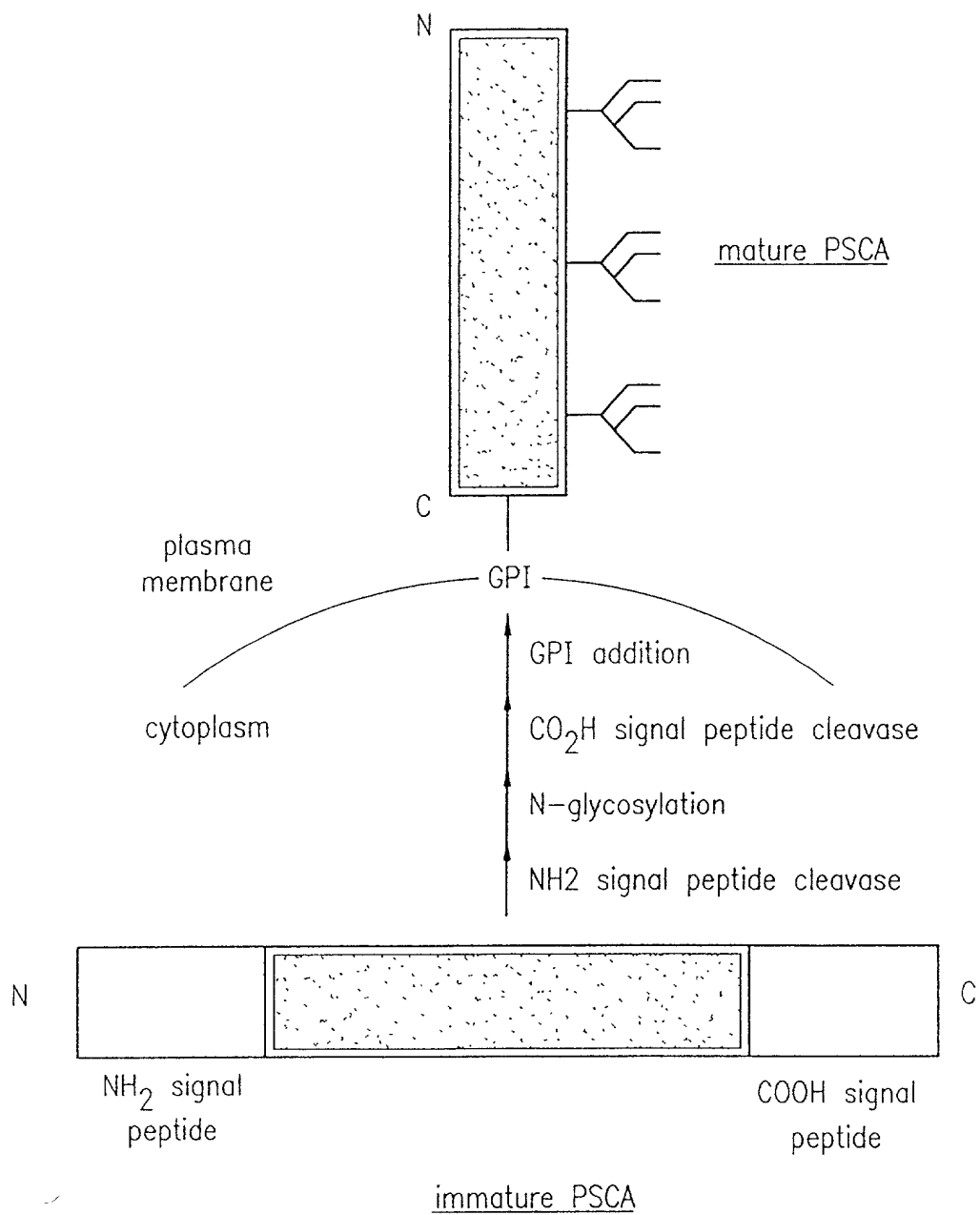


FIG. 16B

FIG. 17

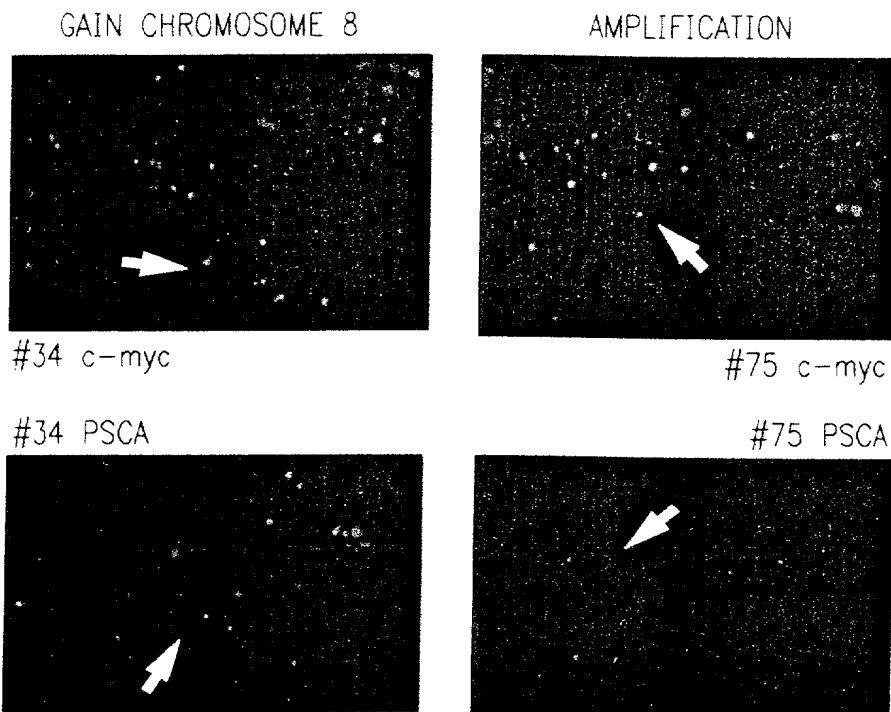
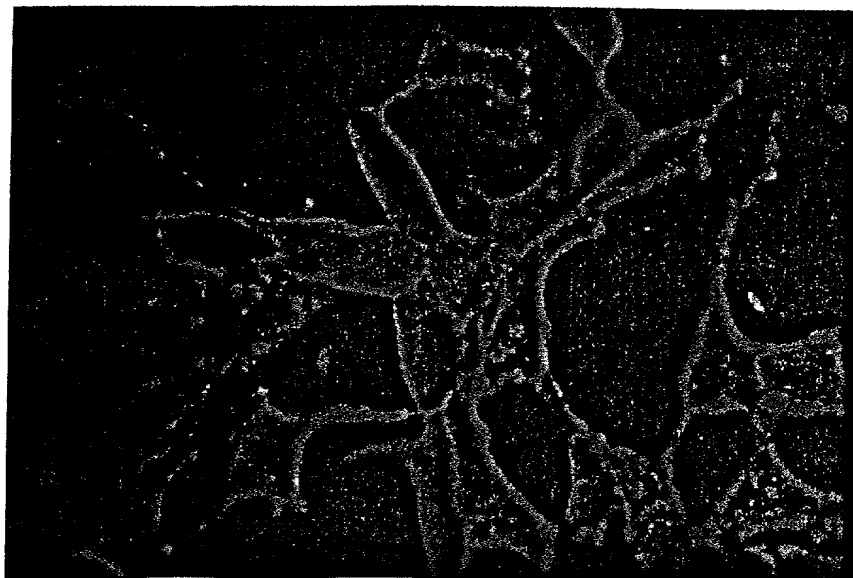


FIG. 18



This image is a dark, grainy, black and white scan, likely of a document page. It is characterized by significant noise and artifacts, including numerous white specks and faint, illegible patterns scattered across the dark background. The overall appearance is that of a low-quality or heavily degraded scan.

FIG. 21

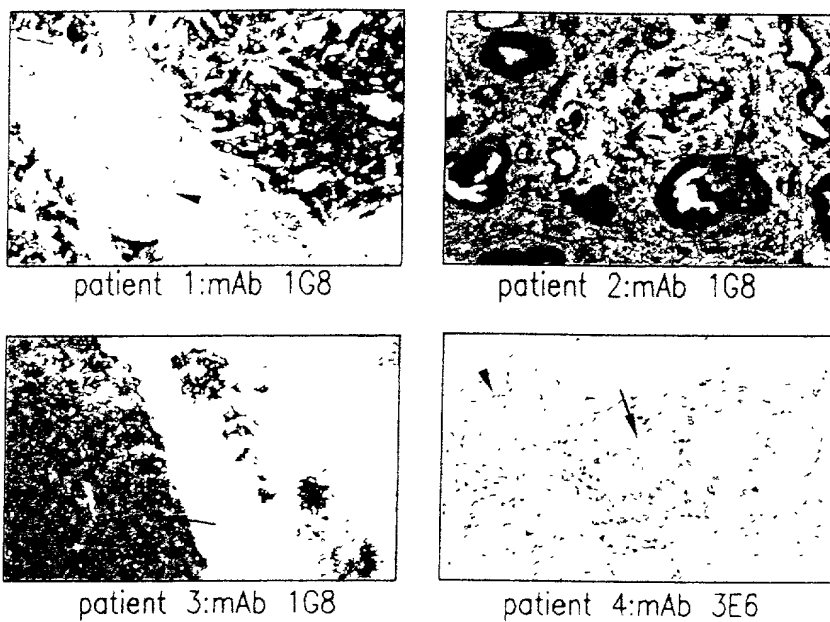
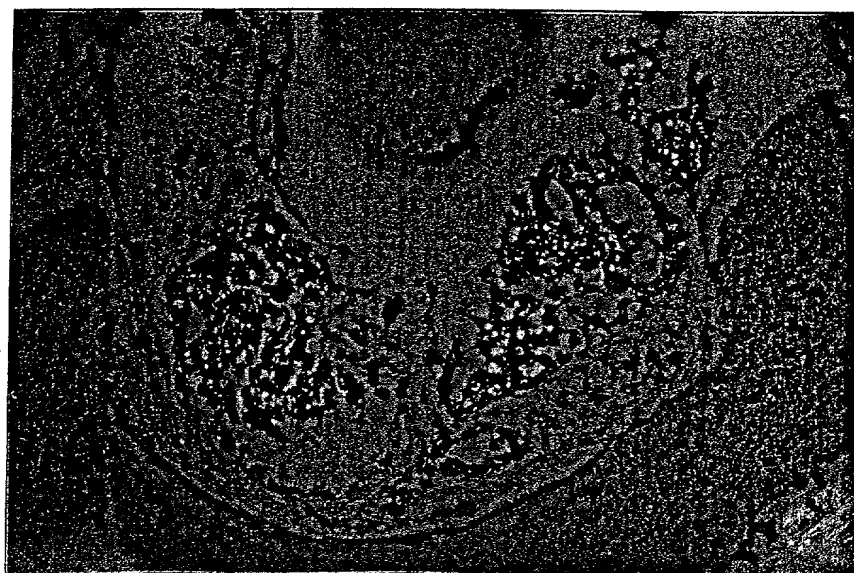


FIG. 22



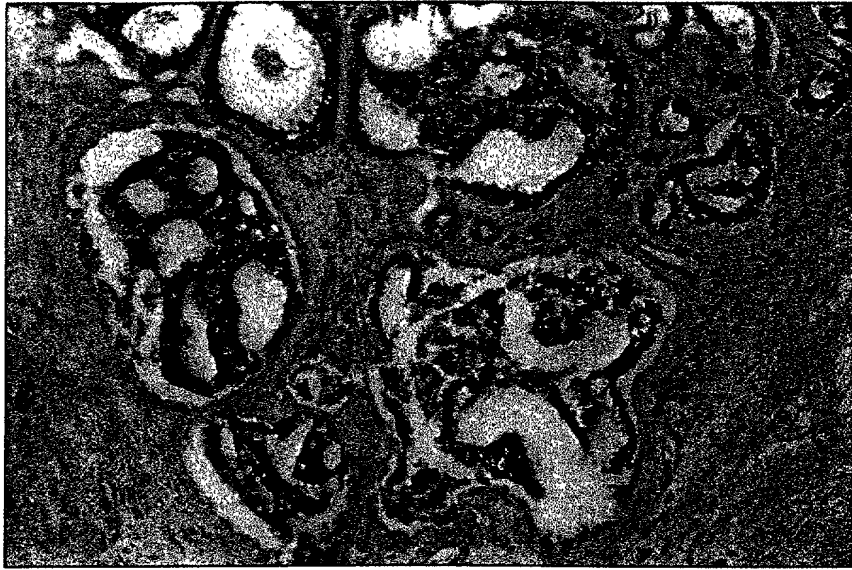


FIG. 23

FIG. 24



[illegible]

FIG. 26

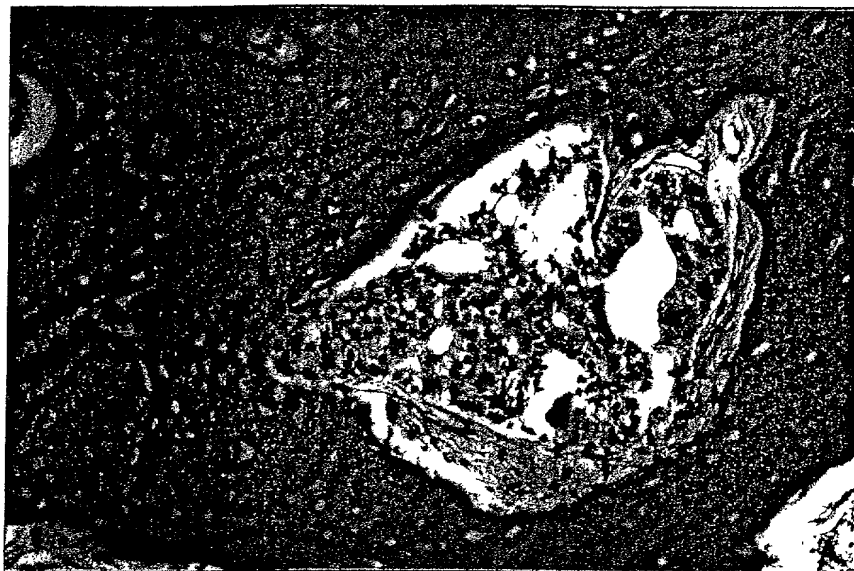
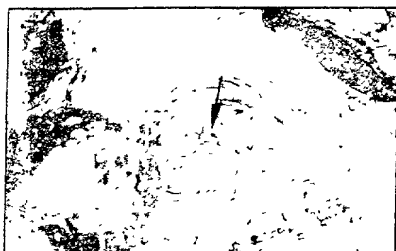
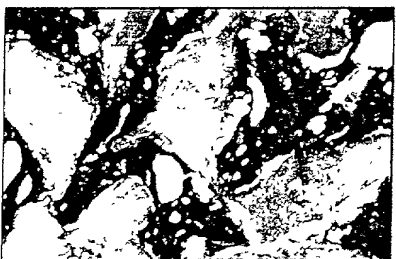


FIG. 27



Patient 5: H and E
and mAb 1G8



Patient 4: H and E
and mAb 3E6

FIG. 28

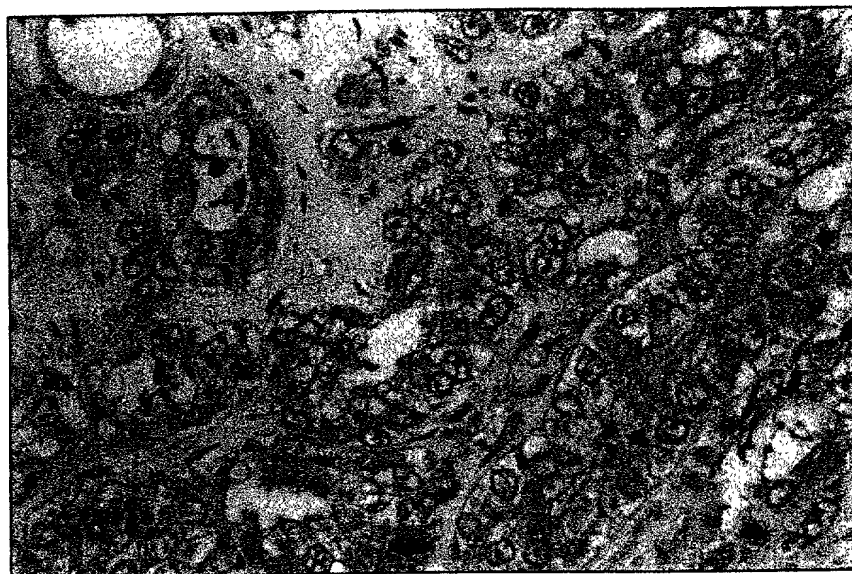
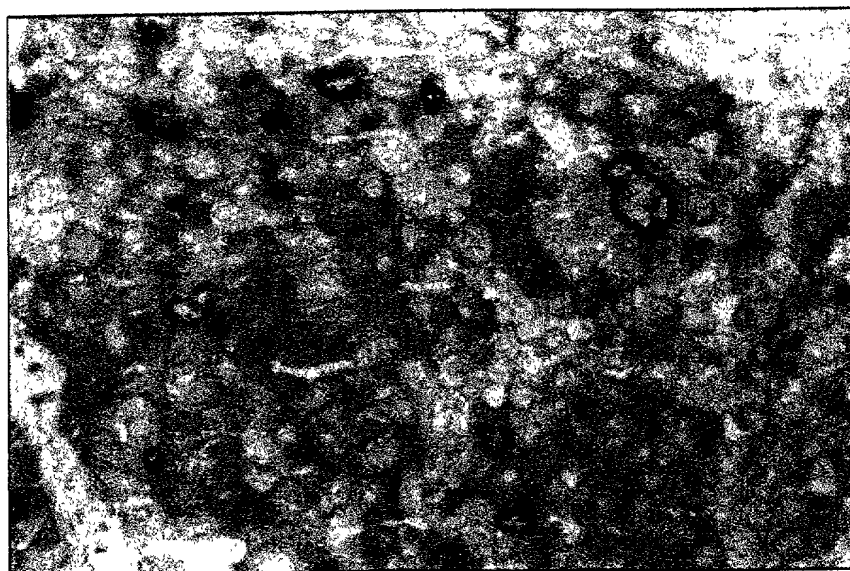


FIG. 29

FIG. 30



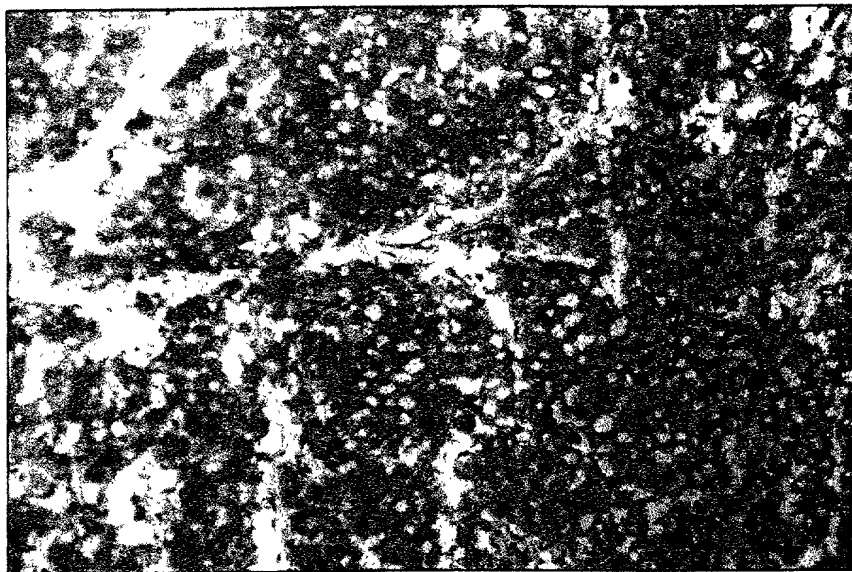


FIG. 31

FIG. 32

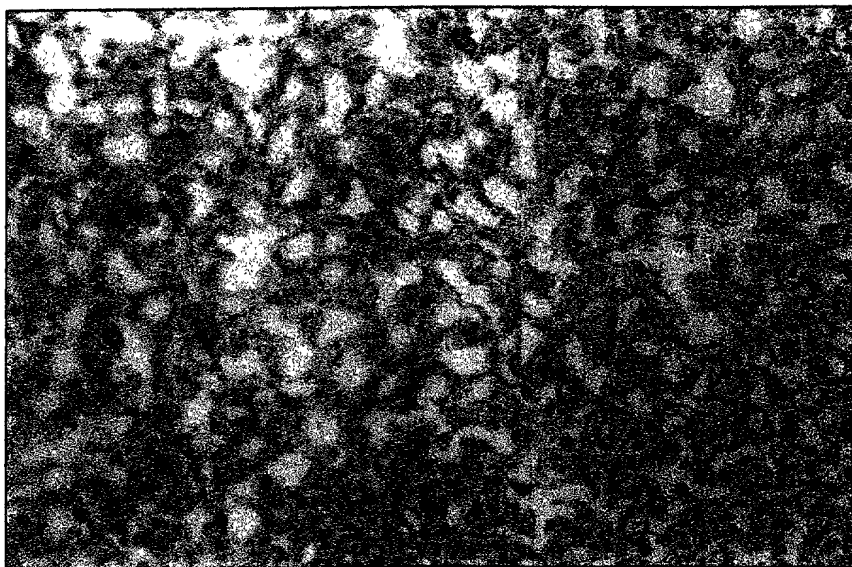


FIG. 33

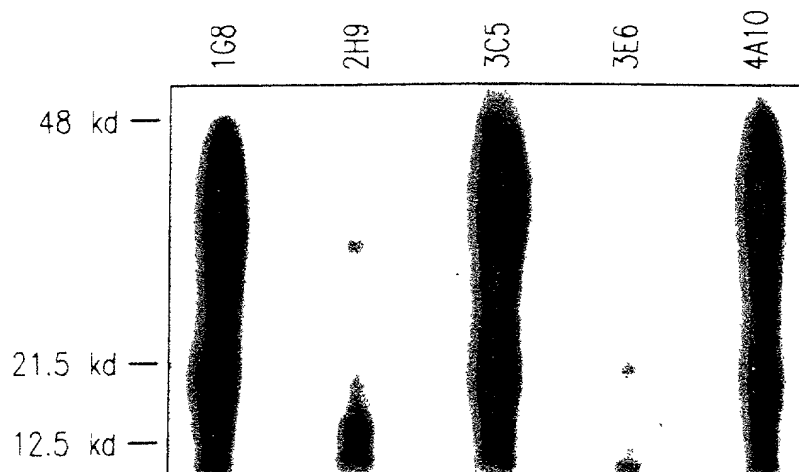
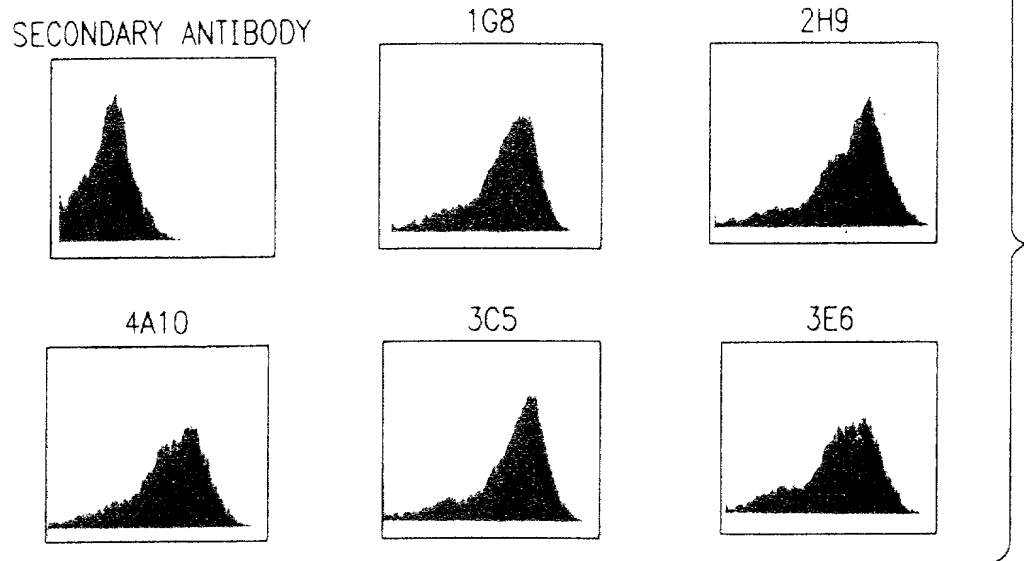


FIG. 34

FIG. 35

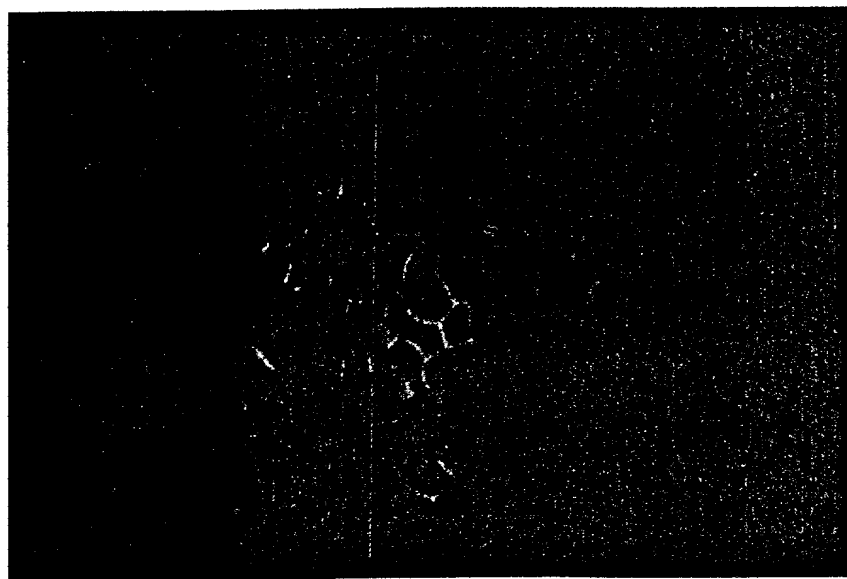
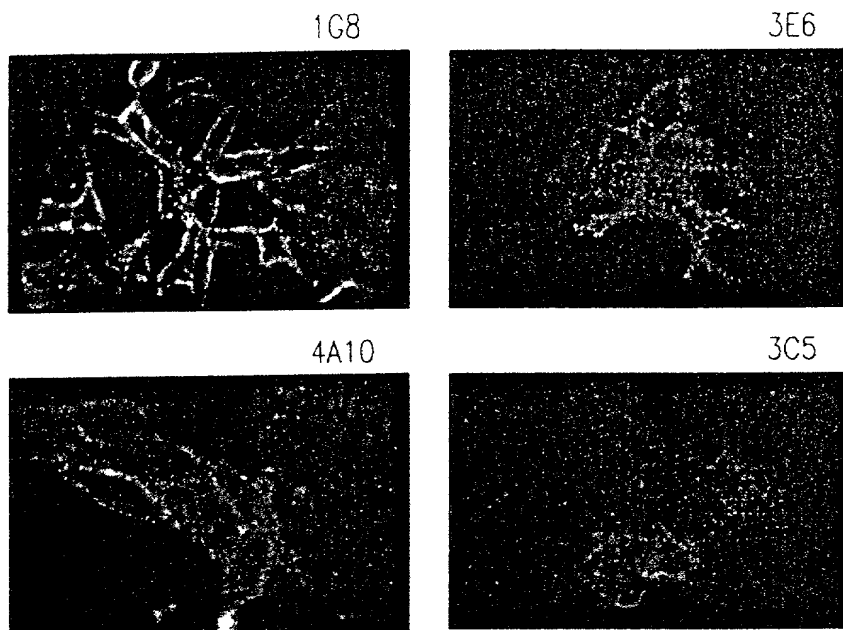


FIG. 36

109220 63455860

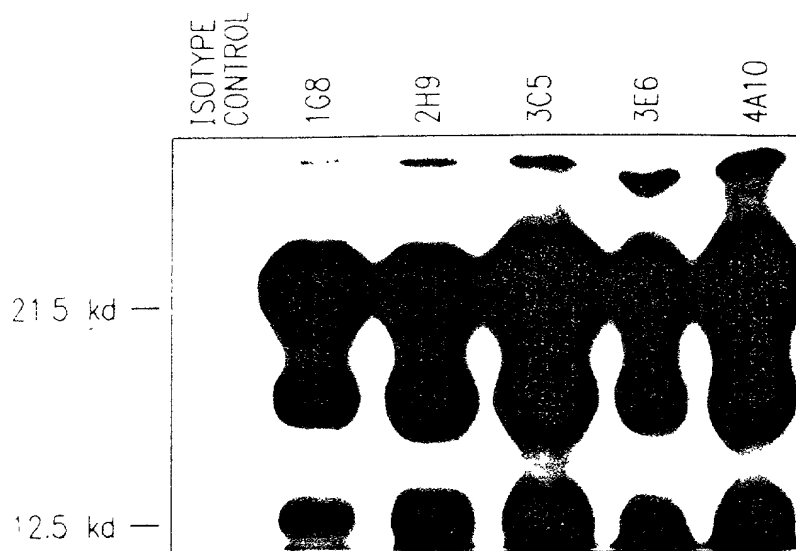


FIG. 37

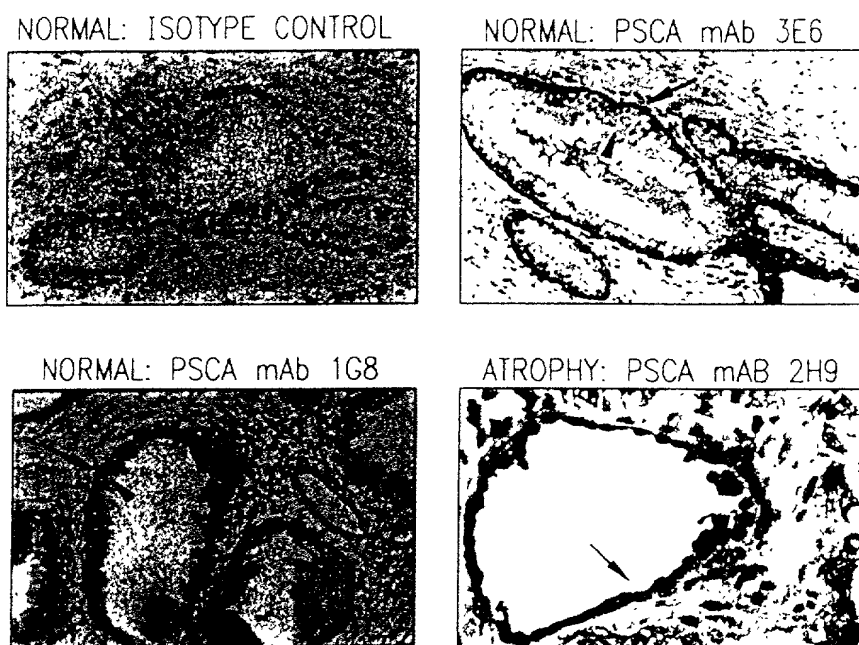
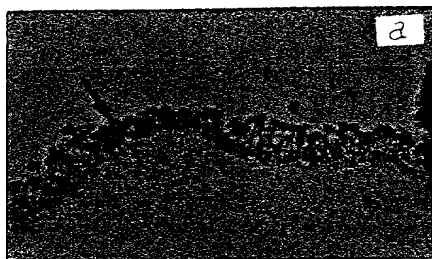
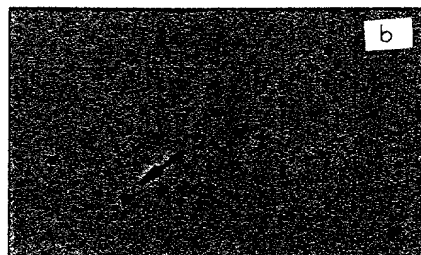


FIG. 38

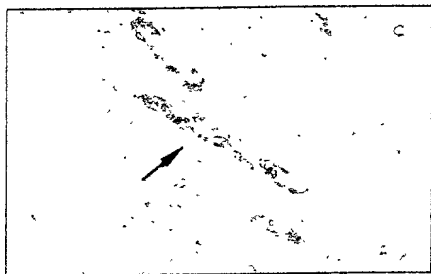
FIG. 39A



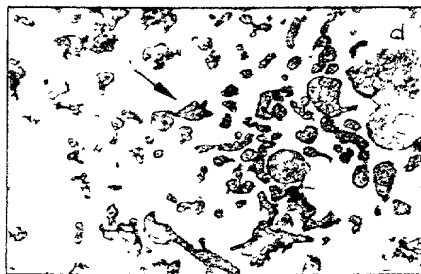
BLADDER: 1G8



COLON: 1G8



KIDNEY: 3E6



PLACENTA: 3E6

PROSTATE

PROSTATE

PROSTATE

KIDNEY

KIDNEY

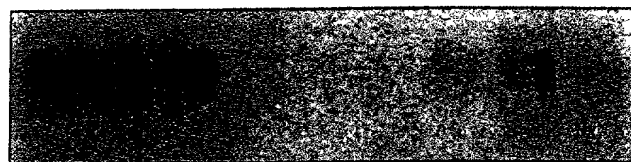
KIDNEY

BLADDER

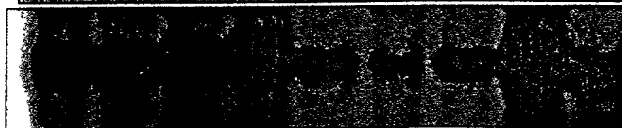
BLADDER

BLADDER

LAPC 9



PSCA



ACTIN

FIG. 39B

40320 6345300

FIG. 40A

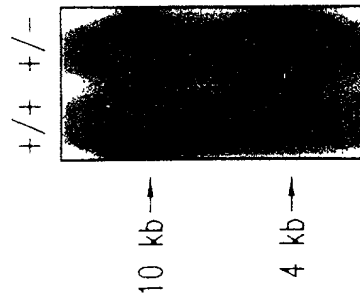
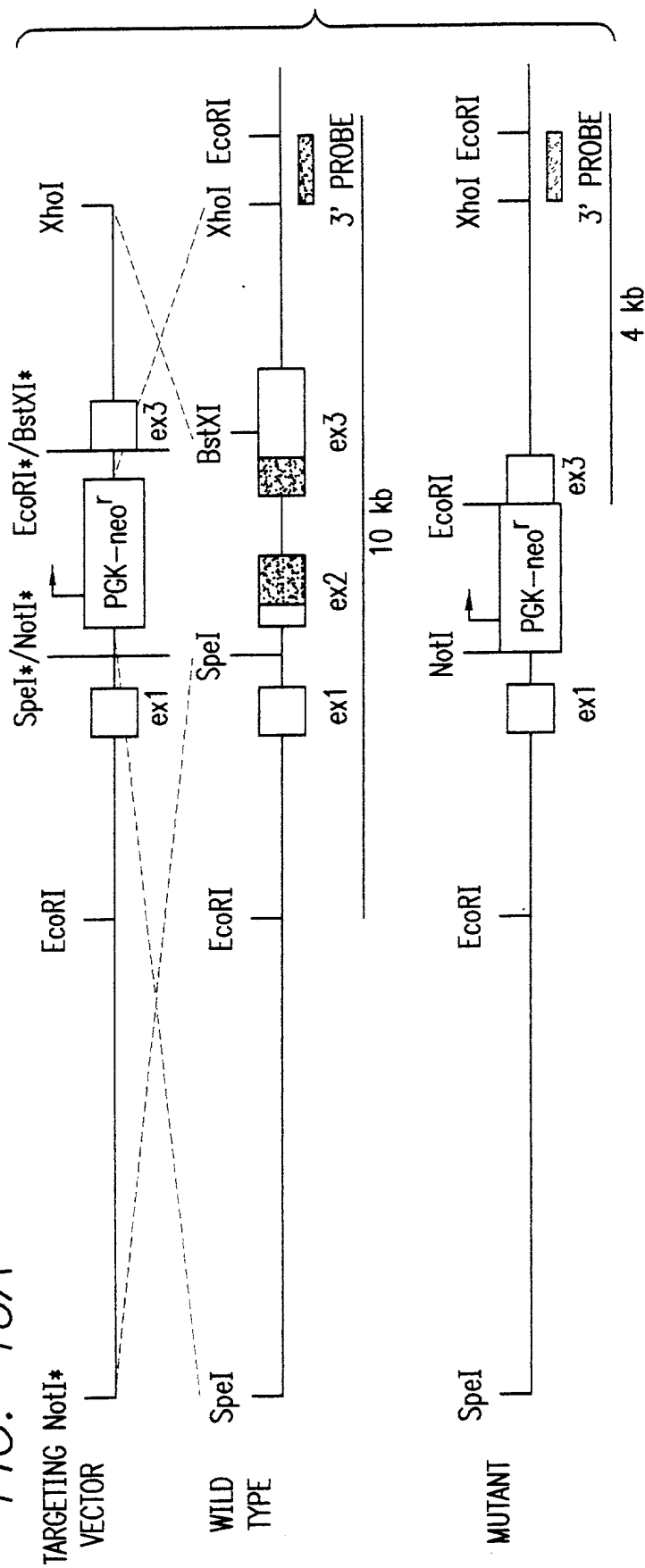
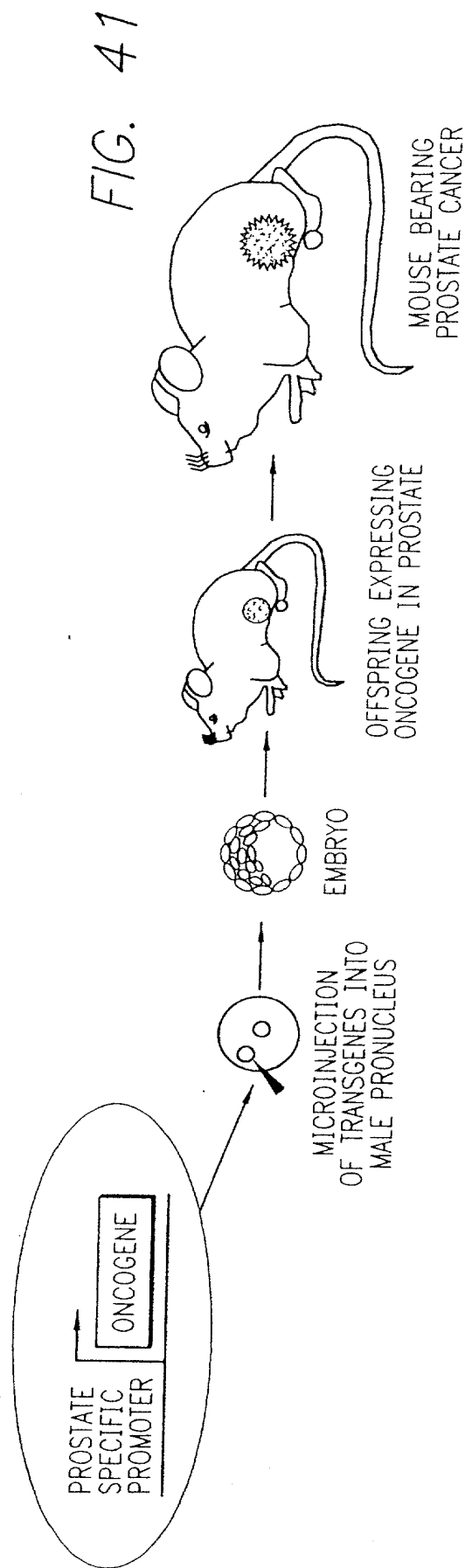


FIG. 40B



TRANSGENE	TARGET TISSUES	CHARACTERISTICS
C3(1) (-3 kb)/ SV40 LARGE+SMALL, T MAROULAKOU et al. 1994 PNAS	PROSTATE (SECRETORY CELLS) URETHRAL, MAMMARY AND SWEAT GLAND	LOW-GRADE PIN 8-12 WKS HIGH-GRADE PIN 8-12 WKS INVASIVE CARCINOMA 28 WKS NO METASTASES
PROBASIN (-426 bp)/ SV40 LARGE+SMALL, T GREENBERG et al. 1995 PNAS	PROSTATE (SECRETORY CELLS)	LOW-GRADE PIN 5-8 WKS HIGH-GRADE PIN 8-12 WKS INVASIVE CARCINOMA 12 WKS METASTASES IN LYMPH NODE, LUNG, LIVER AND BONE
CRYPTIDIN2 (-6.5 kb)/ SV40 LARGE+SMALL, T GARABEDIAN et al. 1998 PNAS	PROSTATE (NEUROENDOCRINE CELLS) SMALL INTESTINE	LOW-GRADE PIN 8-12 WKS HIGH-GRADE PIN 8-12 WKS INVASIVE CARCINOMA 16 WKS METASTASES IN LYMPH NODE, LUNG, LIVER, AND BONE

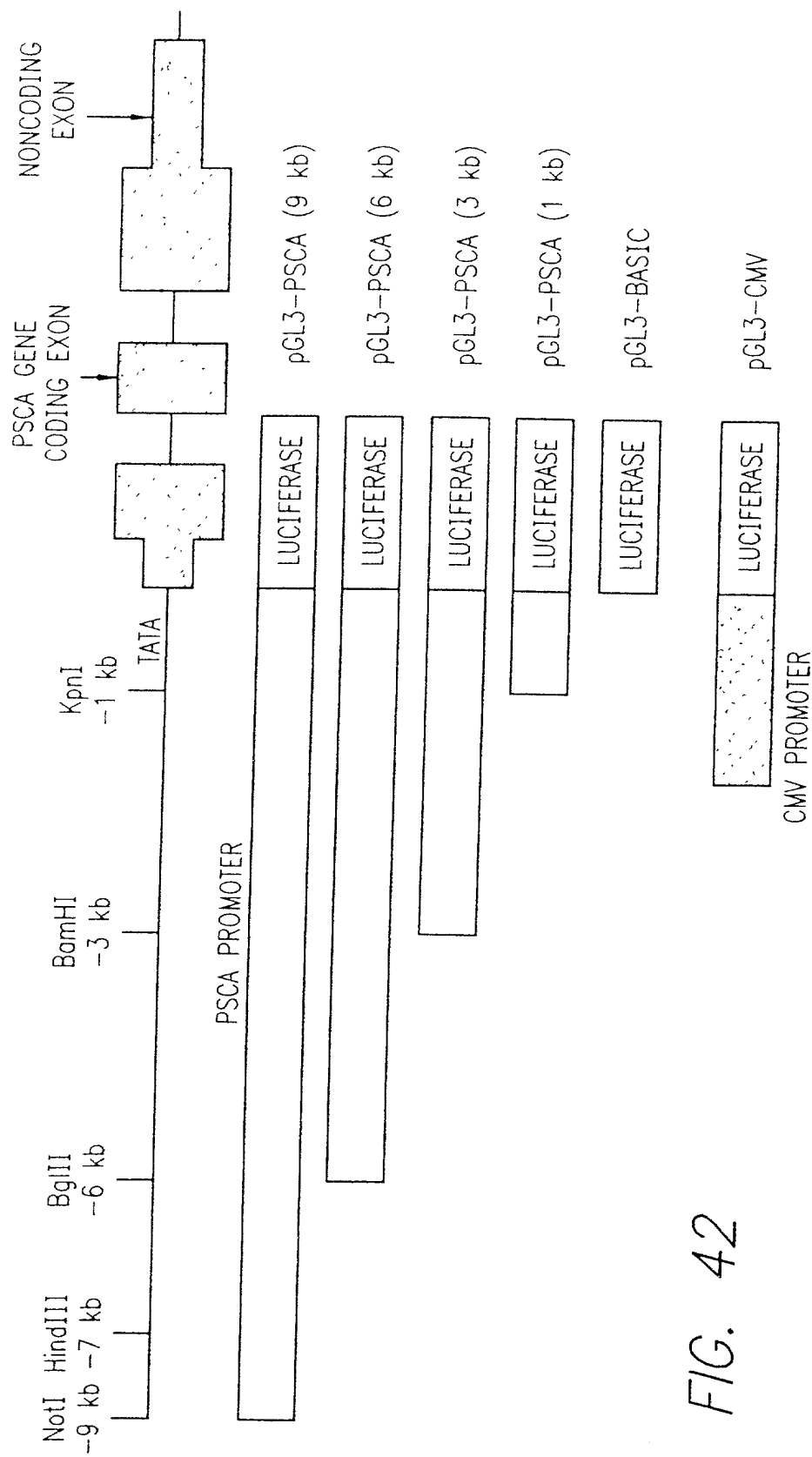


FIG. 42

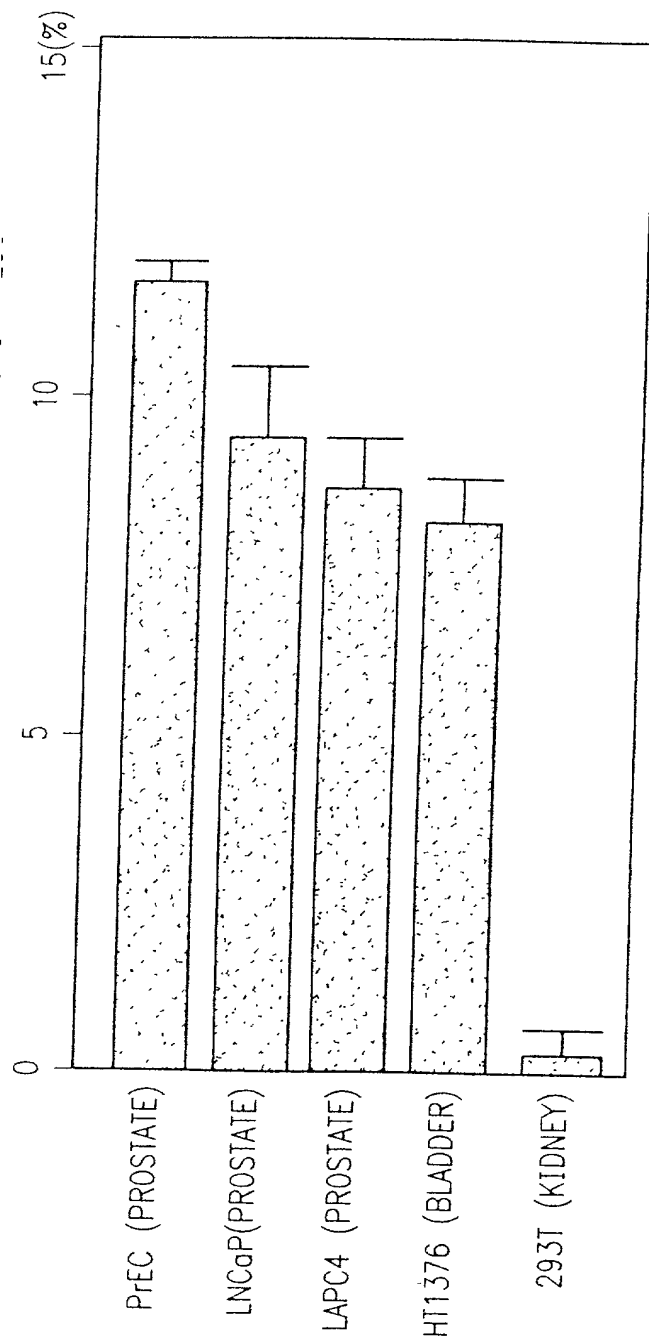


FIG. 43

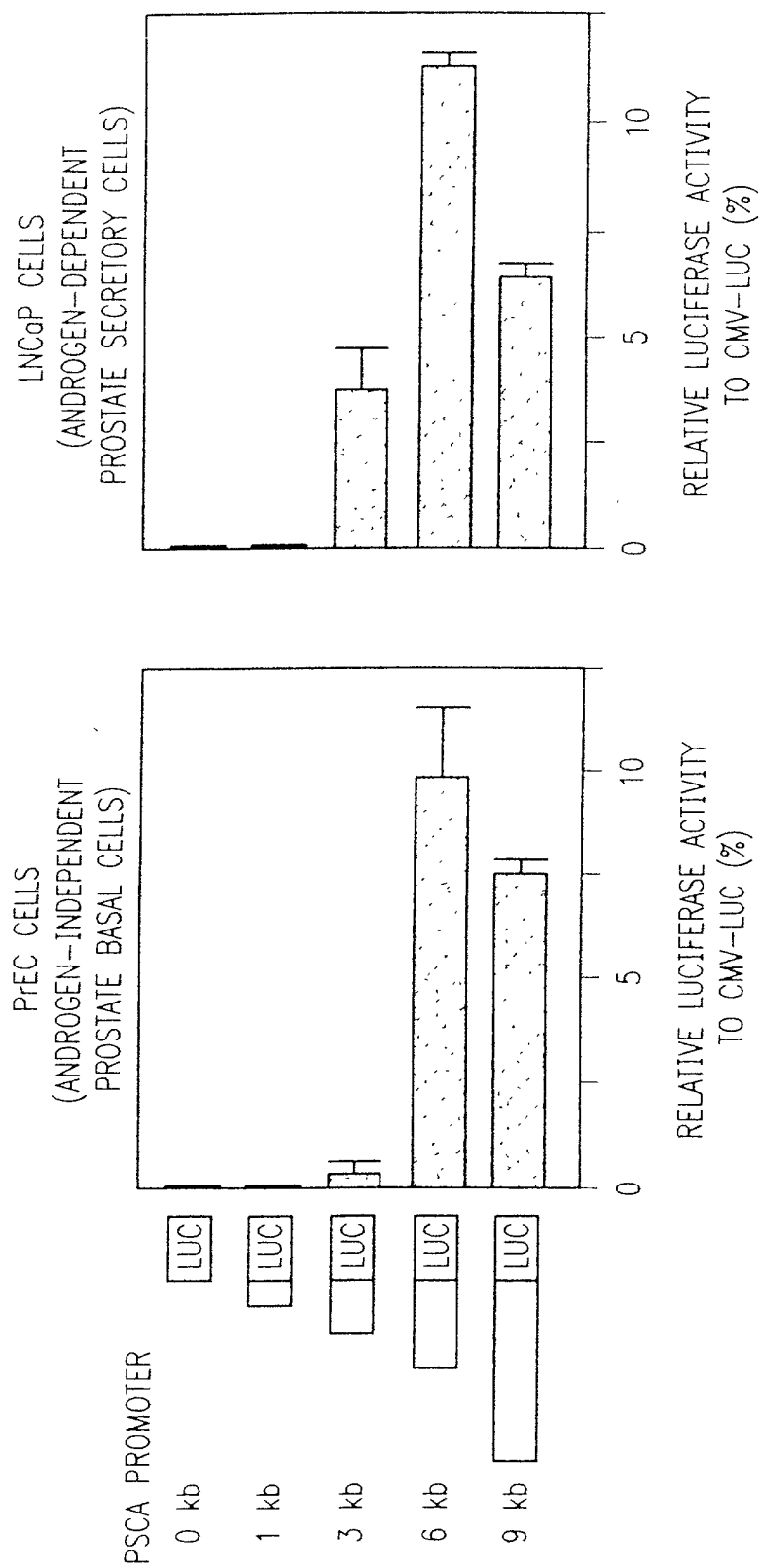
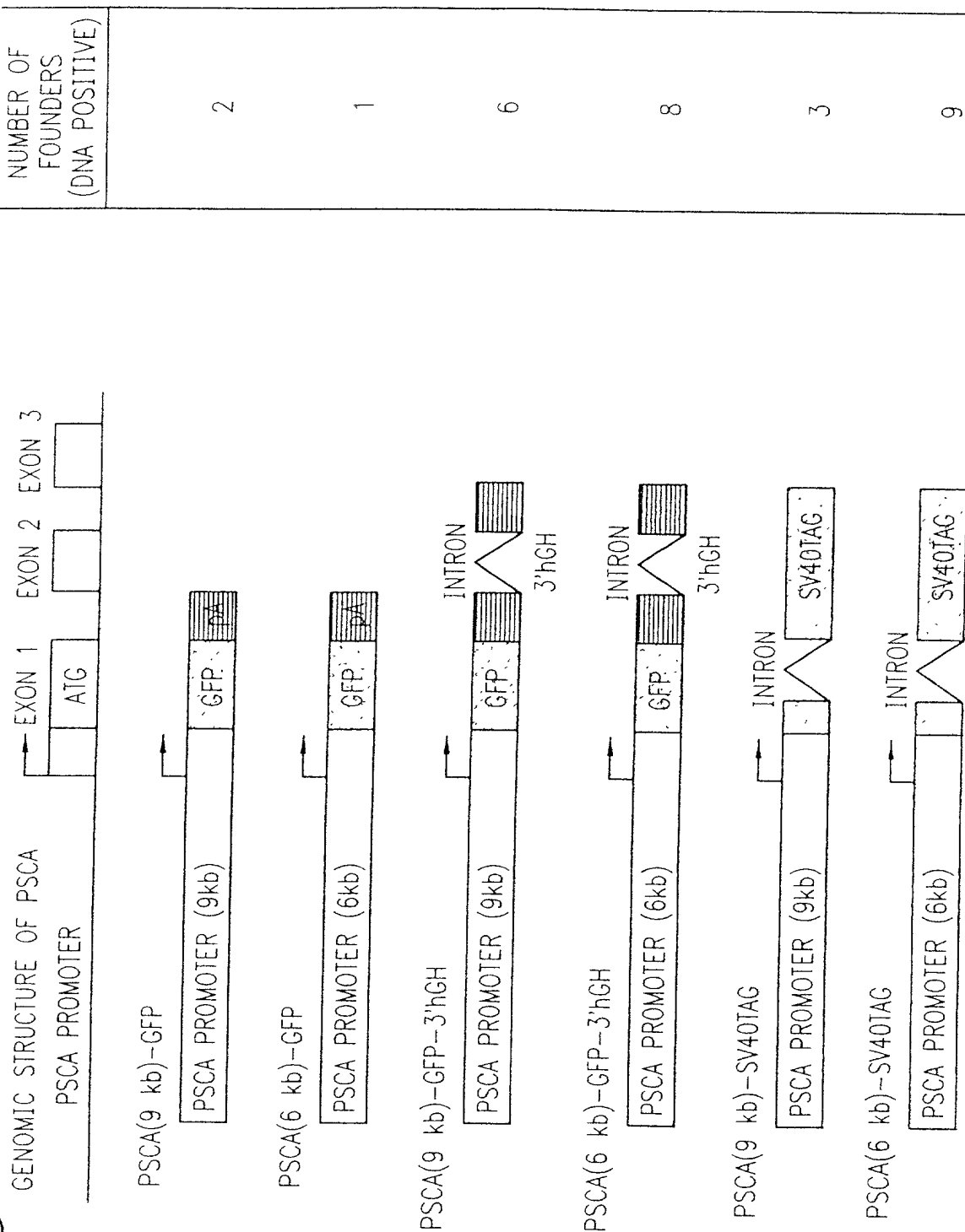


FIG. 44

FIG. 45



NEGATIVE TISSUES

SMALL INTESTINE

SEMINAL VESICLE

TESTS

KIDNEY

BRAIN

SKELETAL MUSCLE

UTERUS

NON-TRANSGENIC

PROSTATE
(A25-106-2)

BLADDER
(A25-104)

SKIN
(A25-106-2)

FIG. 46

403420 " 2343300

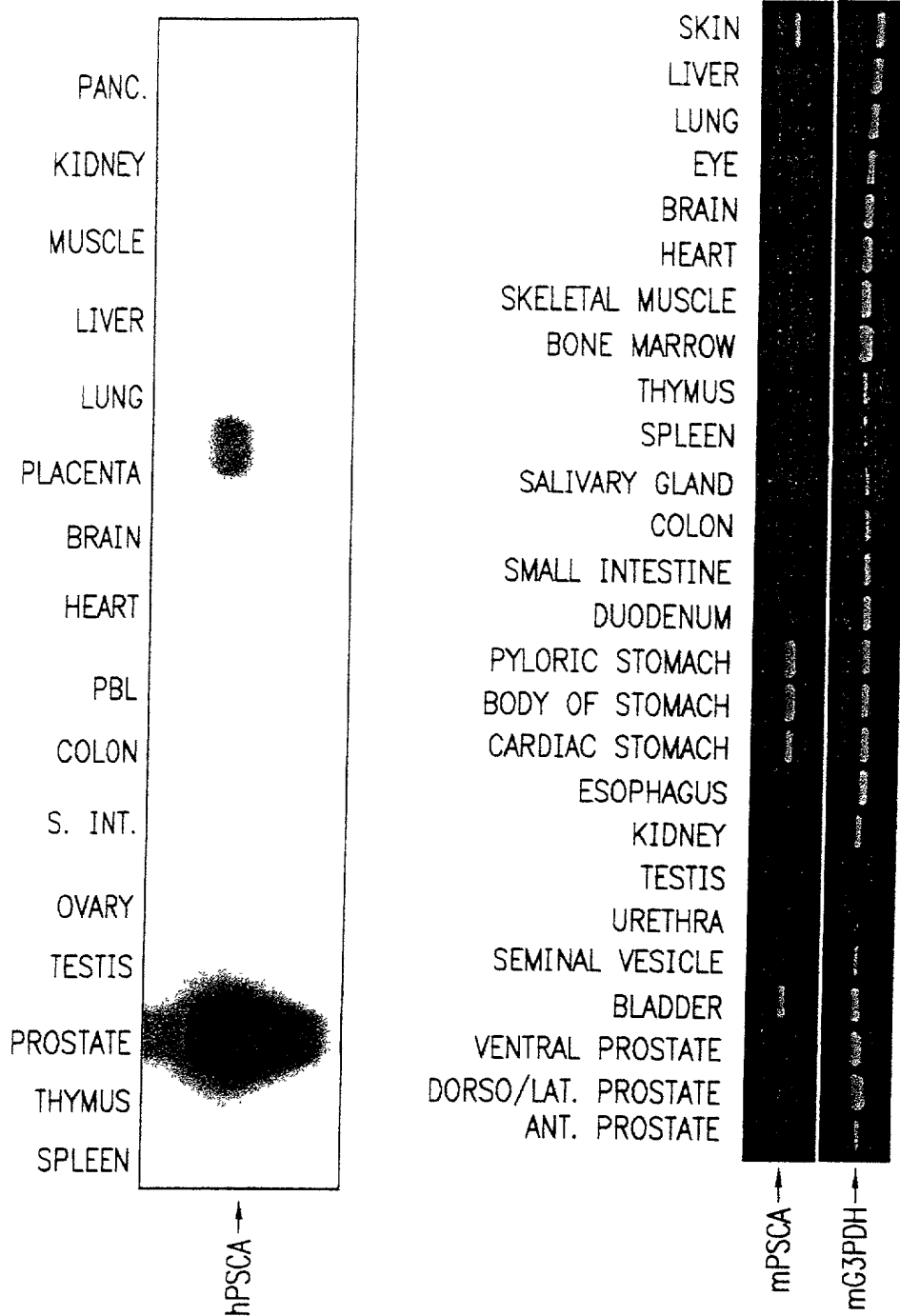


FIG. 47

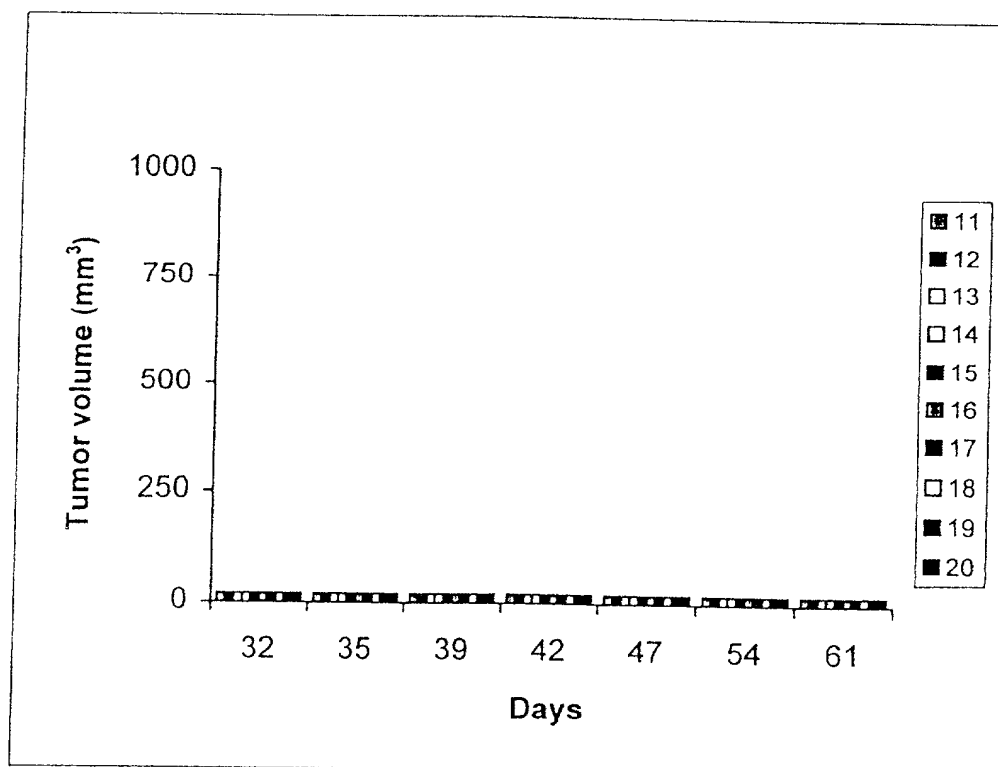
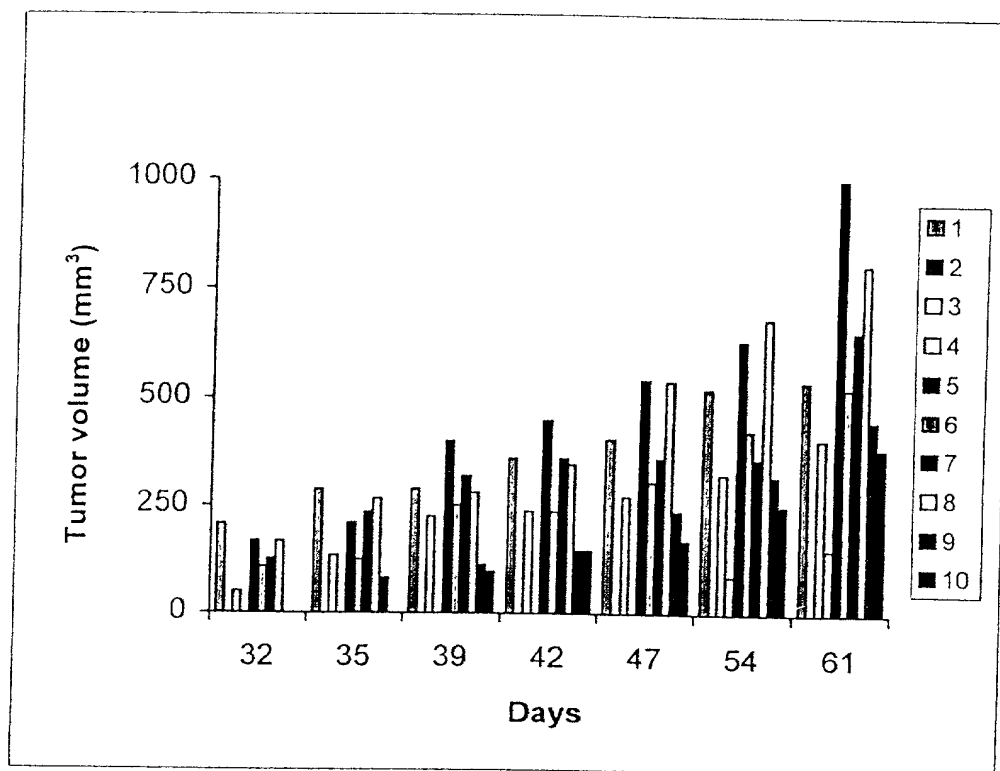
[illegible]

FIG. 49

A

Epitope recognized (OD 450 nm)

mAb	Isotype	F (18-98)	N (2-50)	M (46-109)	C (85-123)
1G8	IgG1 k	1.485	0.004	1.273	0.003
2A2	IgG2a k	0.973	0.631	0.023	0.010
2H9	IgG1 k	1.069	1.026	0.002	0.001
3C5	IgG2a k	1.916	1.709	0.006	0.002
3E6	IgG3 k	1.609	0.036	1.133	2.118
3G3	IgG2a k	2.805	1.731	0.004	0.000
4A10	IgG2a k	1.053	0.493	0.000	0.001

B

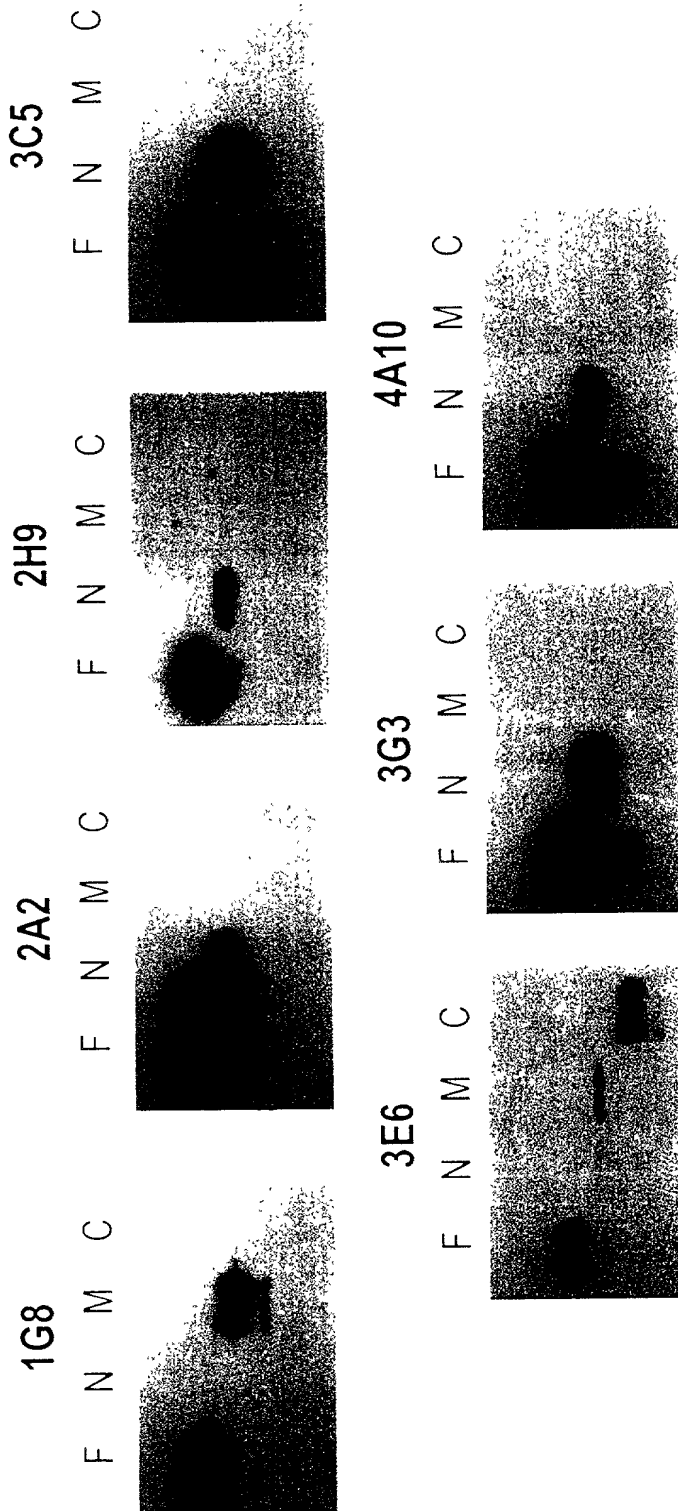
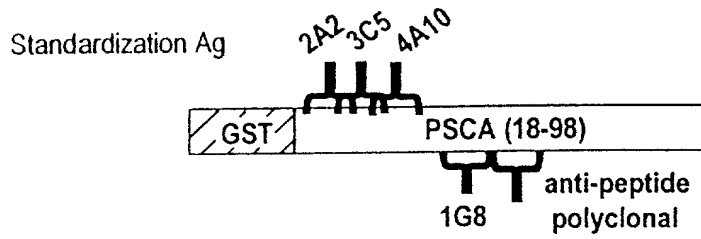
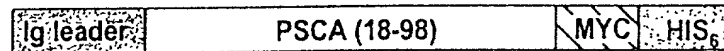


FIG. 50

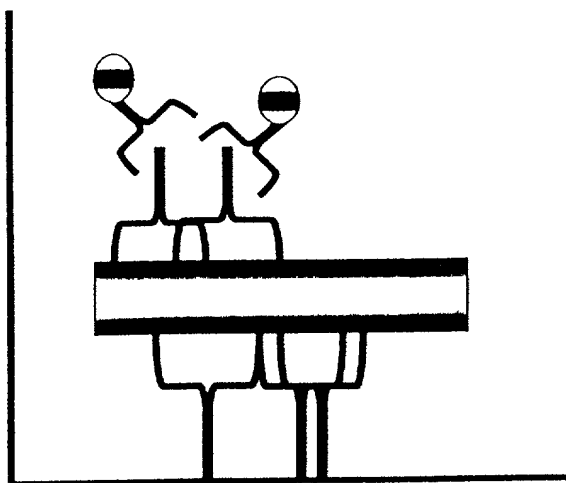
A



Engineered mammalian secreted form



B



Anti-IgG2a HRP

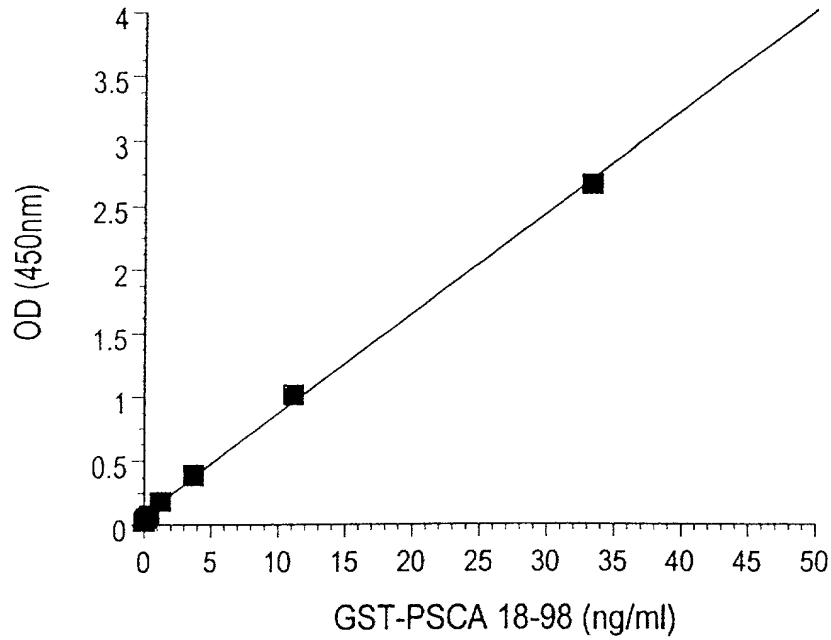
Anti-PSCA mAbs 3C5+4A10+2A2 (IgG2a)

PSCA

Affinity purified anti-peptide polyclonal
+ mAb 1G8 (IgG1)

FIG. 51

A



B

Sample	OD+range (n=2)	ng/ml
vector	0.005+0.001	ND
vector+hu serum	0.004+0.001	ND
secPSCA	2.695+0.031	32.92
secPSCA+hu serum	2.187+0.029	26.55

FIG. 52

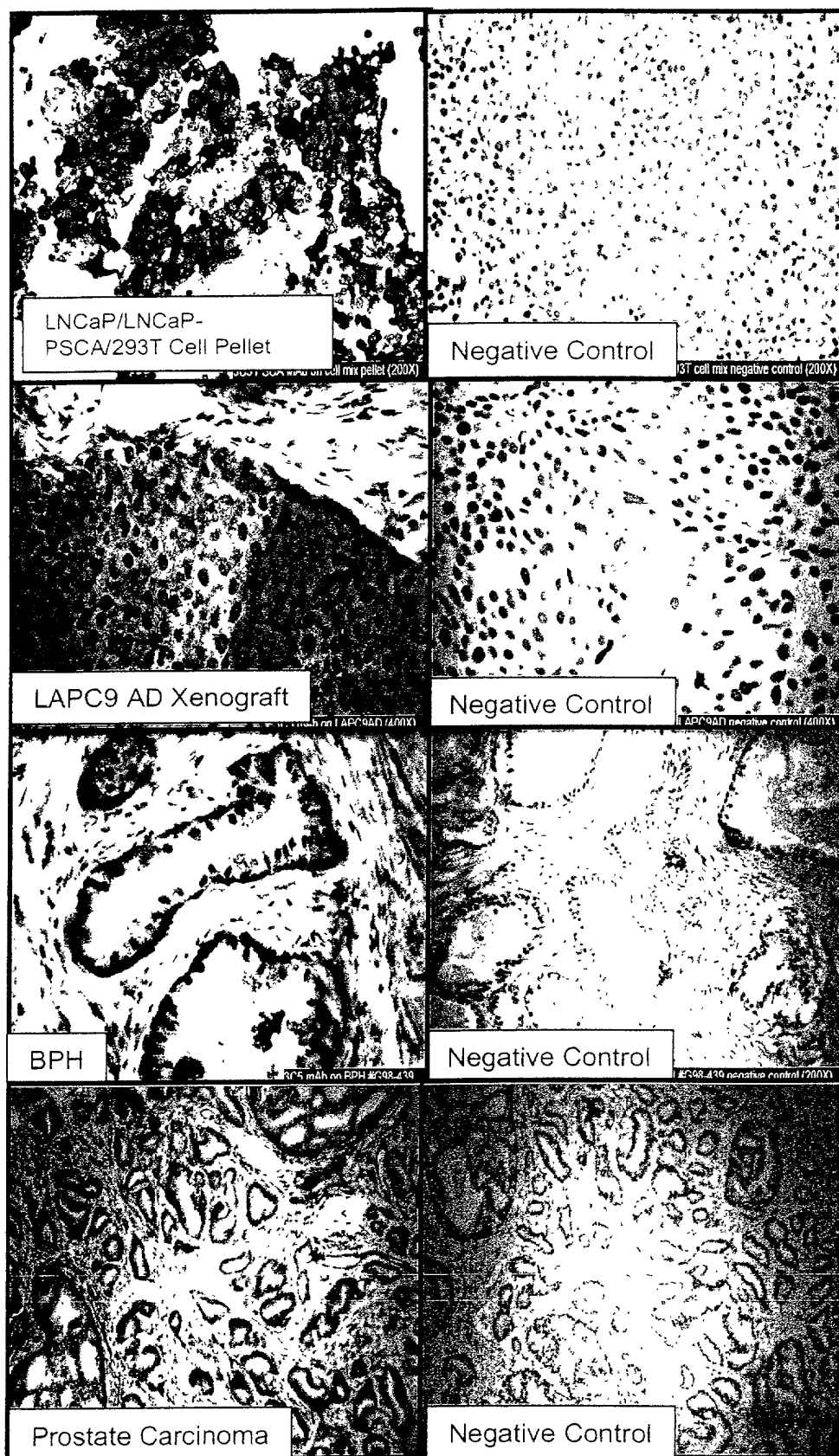


FIG. 53

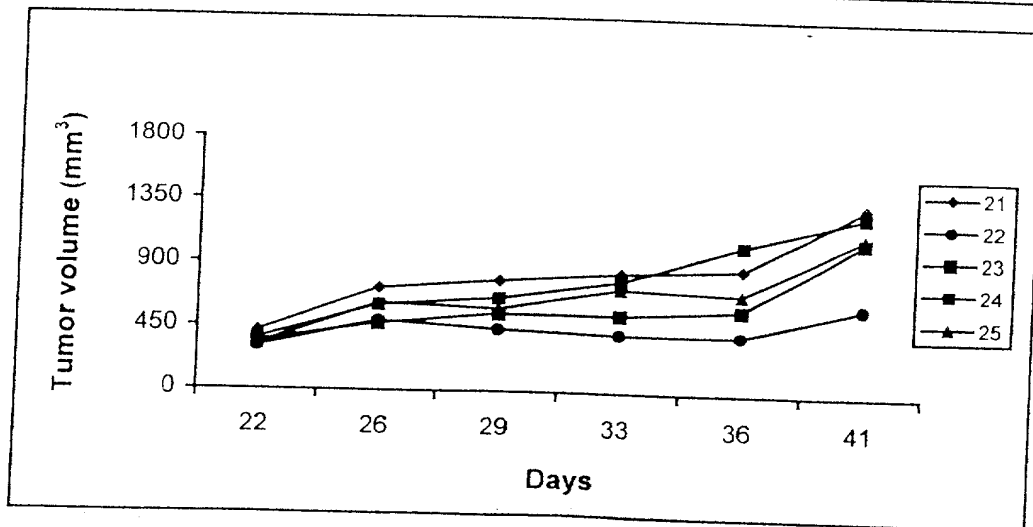
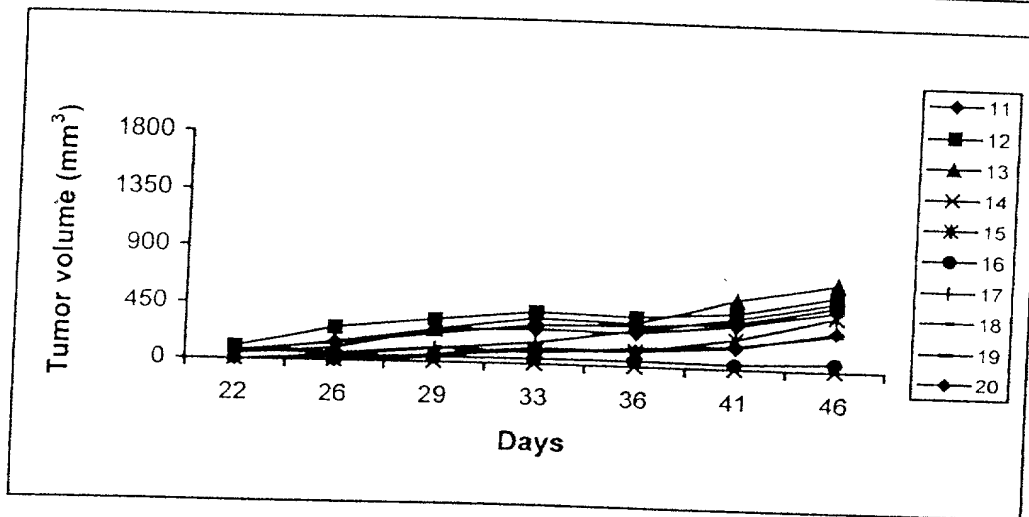
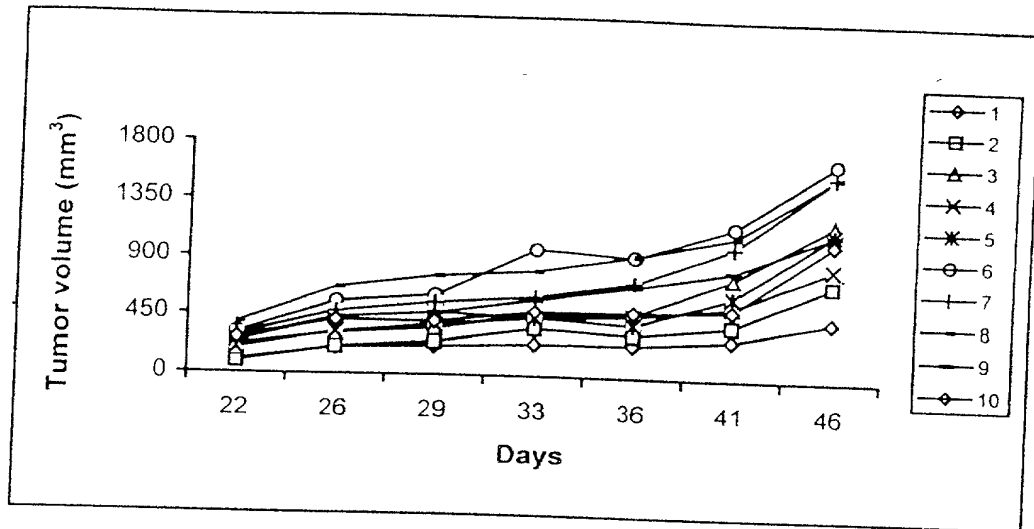


FIG. 54

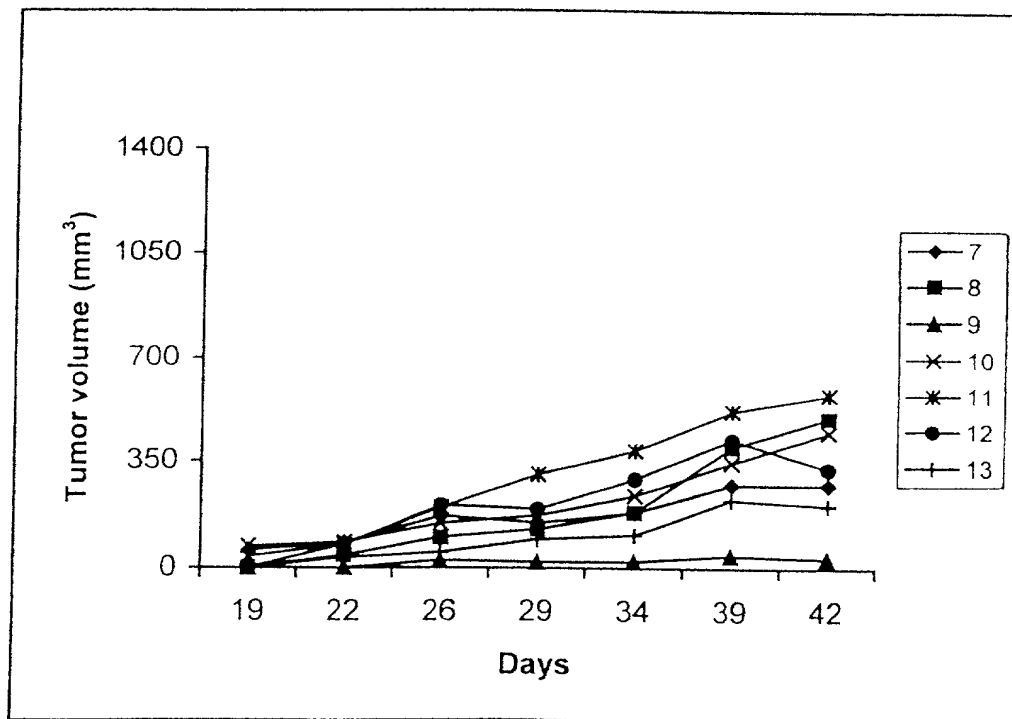
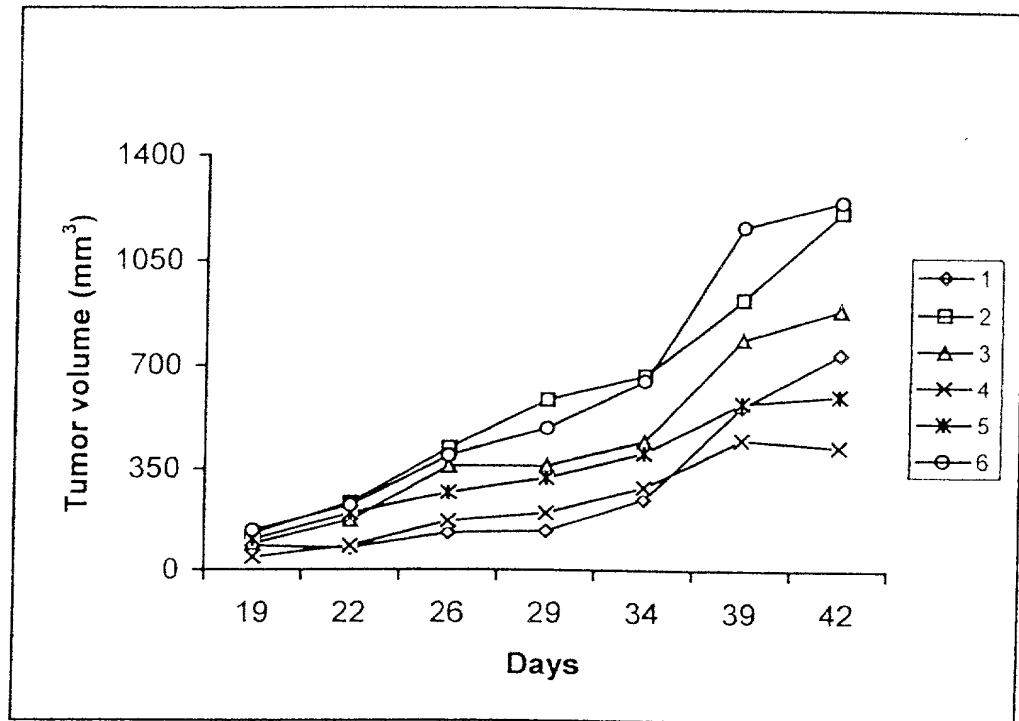


FIG. 55

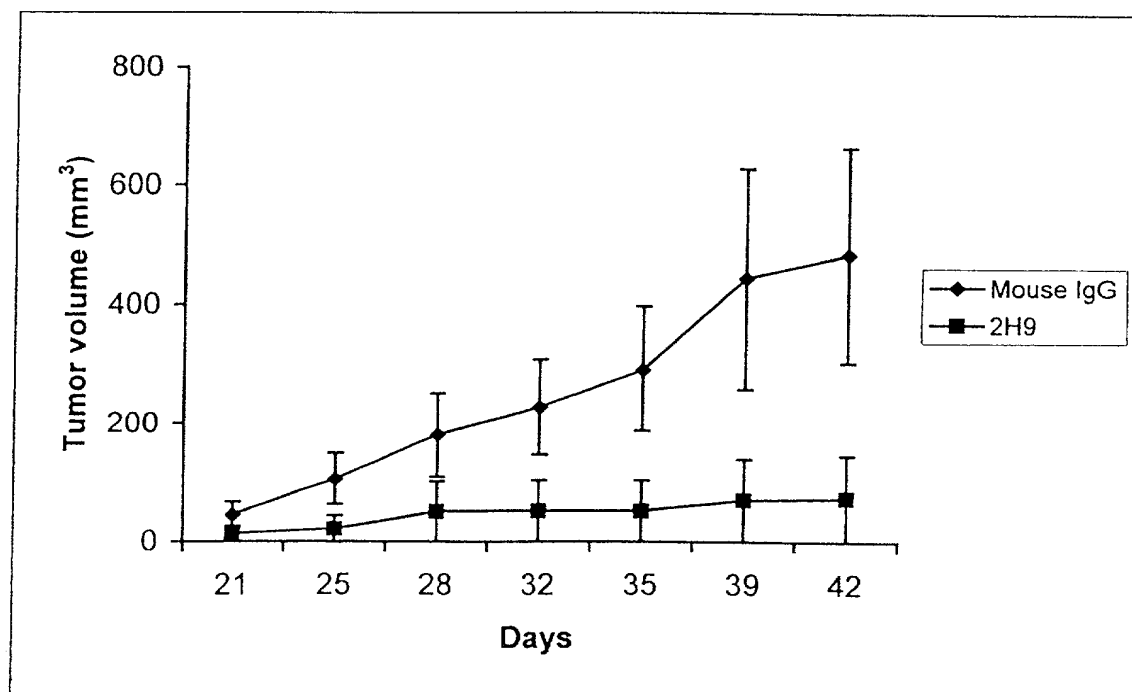
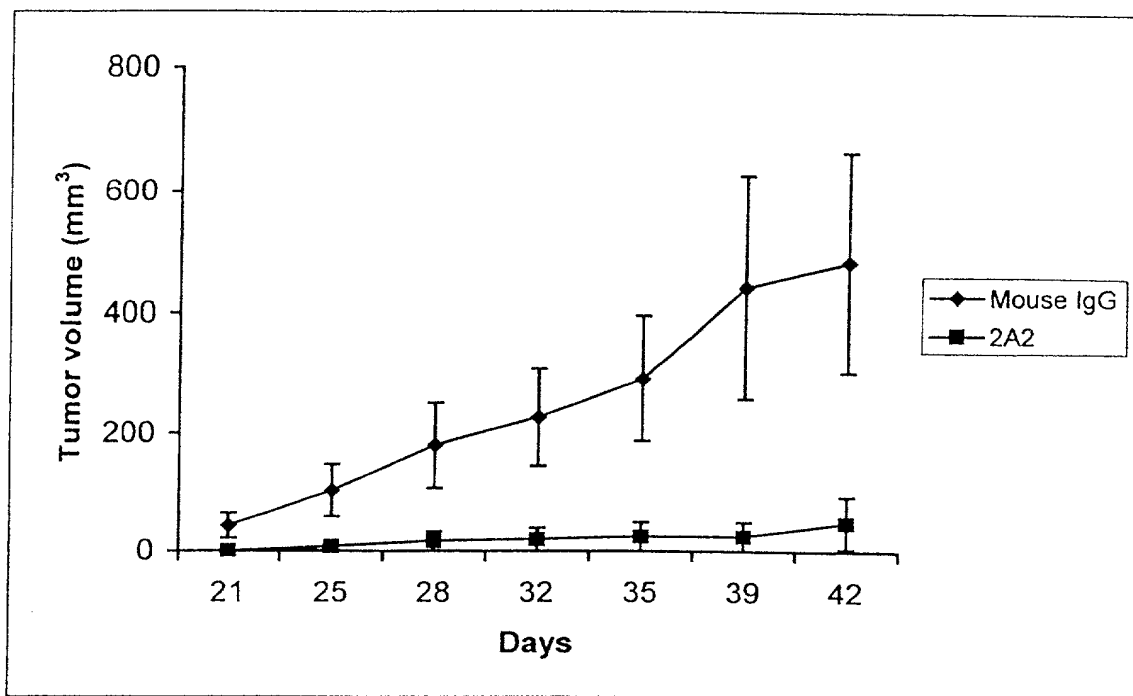


FIG. 56

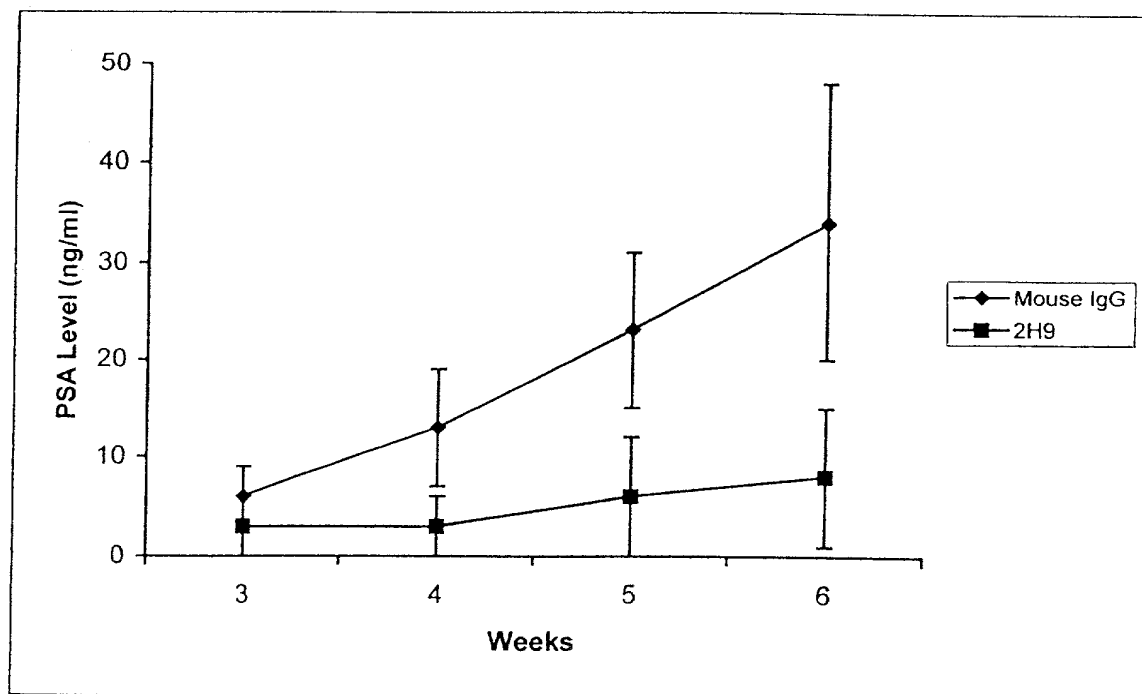
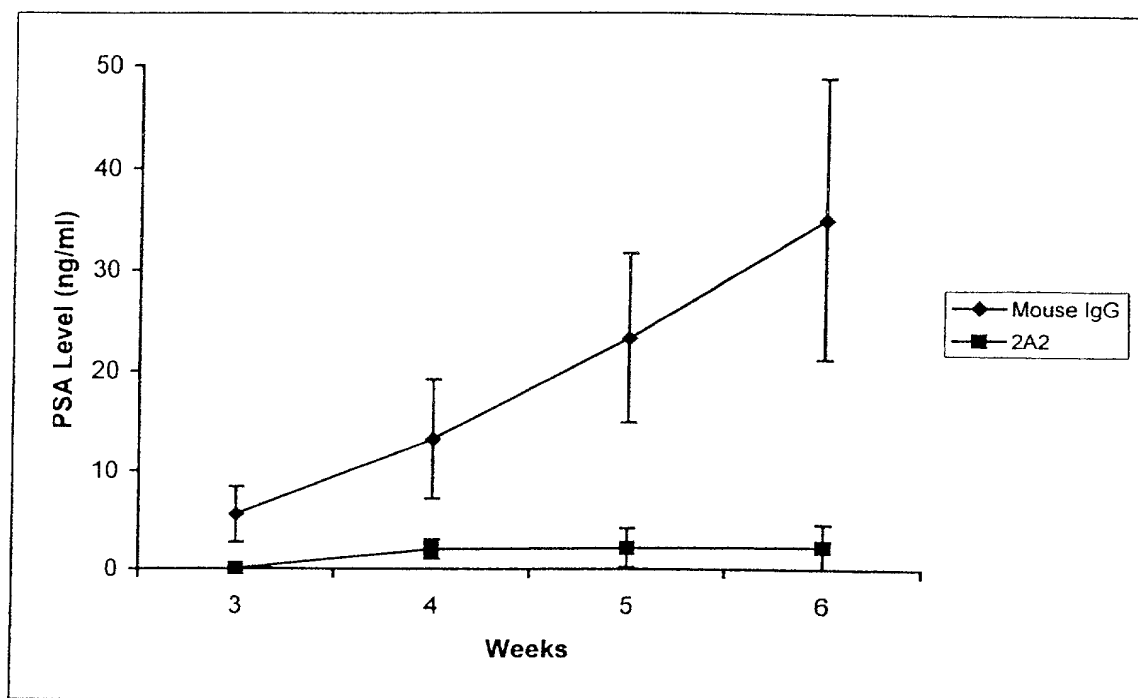


FIG. 57

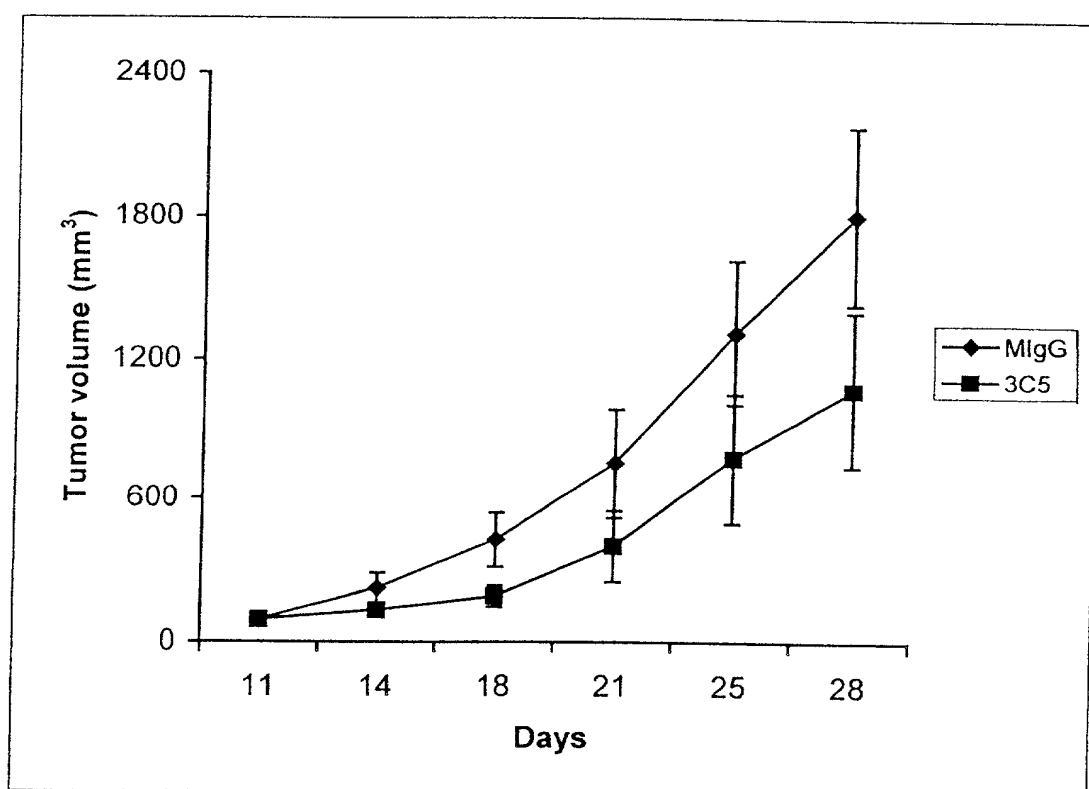


FIG. 58

TGCTTCTTCCTGATGGCAGTGGTTATAGGAGTCAATTCAAGAGTTCAAGTGCAGCAGTCT 60
 C F L M A V V I G V N S E V Q L Q Q S 20

 GGGCAGAACTTGTGAGTCAAGGCGCTCAGTCAAGTTGTCCTGCACAGCTTCTGGCTTC 120
 G A E L V R S G A S V K L S C T A S G F 40

 CDR1
 AACATTAAAGACTACTATATACACTGGGTGAATCAGAGGCGCTGACCAGGCGCTGGAGTGG 180
 N I K D Y Y I H W V N Q R P D Q G L E W 60

 CDR2
 ATTGGATTGGATTCCTGAGAAATGGTGACACTGAATTTGTCCGAAGTTCCAGGGCAAG 240
 I G W I D P E N G D T E F V P K F Q G K 80

 GCCACTATGACTGCAGACATTTTCTCCAAACACAGCGCTACCTGCACCTCAGCAGCCTGACA 300
 A T M T A D I F S N T A Y L H L S S L T 100

 CDR3
 TCTGAAGACACTGCCGTCTATTAAGTAAACGGGGGTTTCTGGGGCCAAAGGACTCTG 360
 S E D T A V Y Y C K T G G F W G Q G T L 120

 GTCACGTGTCTGTGAGCCAAACGACACCCCCCATCTGTCTATCCACTG
 V T V S A A K T T P P S V Y P L

FIG. 59

TTGGTAGCAACAGCCCTCAGATGTCCACTCCAGGTCCAAGTGCAGCAACCTGGGTCTGAA 60
L V A T A S D V H S Q V Q L Q Q P G S E 20

CTGGTGAGGCCTGGAACCTCAGTGAAGCTGTCTGCAAGGCTTCTGGCTATACATTCTCC 120
L V R P G T S V K L S C K A S G Y T F S 40
CDR1

AGCTACTGGATGCACTGGGTGAAGCAGAGGCGCTGGACAAGGCGCTTGAGTGGATTGGAAT 180
S Y W M H W V K Q R P G Q G L E W I G N 60

ATTGACCCTGGTAGTGGTTACACTAACTACGCTGAGAACCTCAAGACCAGGCCACACTG 240
I D P G S G Y T N Y A E N L K T K A T L 80
CDR2

ACTGTAGACACATCCTCCAGCACAGCCTACATGCAGCTCAGCAGCCTGACATCTGAGGAC 300
T V D T S S S T A Y M Q L S S L T S E D 100

TCTGCAGTCTATTACTGTACAAGCCGATCTACTATGATTACGACGGGATTTGCTTACTGG 360
S A V Y Y C T S R S T M I T T G F A Y W 120
CDR3

GGCCAAGGGACTCTGGTCACTGTCTCTGCAGCTACAACAGCCCCCATCTGTCTATCCA 420
G Q G T L V T V S A A T T T A P S V Y P 160

CTGGCC
L A

FIG. 60

AATGACTTCGGGTTGAGCTGGGTTTTTATTATTGTTCTTTTAAAGGGTCCGGAGTGAA 60
N D F G L S W V F I I V L L K G V R S E 20

GTGAGGCTTGAGGAGTCTGGAGGAGGCTGGTGCAACCTGGAGGATCCATGAAACTCTCC 120
V R L E E S G G G W V Q P G G S M K L S 40

TGTTAGCCTCTGGATTACTTTTCAGTAATTACTGGATGACTTGGTCCGCCAGTCTCCA 180
C V A S G F T F S N Y W M T W V R Q S P 60
CDR1

GAGAAGGGCTTGAGTGGTGTGCTGAAATTCGATTGAGATCTGAAATTTATGCAACACAT 240
E K G L E W V A E I R L R S E N Y A T H 80
CDR2

TATGCGGAGTCTGTGAAAGGGAAATTCACCATCTCAAGAGATGATTCAGAAAGTCGTCTC 300
Y A E S V K G K F T I S R D D S R S R L 100

TACCTGCAAAATGAACAACTTAAGACCTGAAGACAGTGGAATTTATTACTGTACAGATGGT 360
Y L Q M N N L R P E D S G I Y Y C T D G 120

CTGGACGACCTAACTGGGGCCAGGGACTCTGGTCACTGTCTCTGCAGCCAAAACGACA 420
L G R P N W G Q G T L V T V S A A K T T 140
CDR3

CCCCCATCTGTCTATCCACTGGCCCCCTTGTGTA
P P S V Y P L A P C V

FIG. 61

CDR1 Comparisons

1G8	1gG _{1k}	Middle	G	F	N	I	K	D	Y	Y	I	H
2H9	1gG _{1k}	N-Term.	G	F	T	F	S	N	Y	W	M	T
4A10	1gG _{2ak}	N-Term.	G	Y	T	F	S	S	Y	W	M	H

CDR2 Comparisons

1G8	1gG _{1k}	W	I	D	P	E	N	G	D	T	E	F	V	P	K	F	Q	G		
2H9	1gG _{1k}	E	I	R	L	R	S	E	N	Y	A	T	H	Y	A	E	S	V	K	G
4A10	1gG _{2ak}	N	I	D	P	G	S	G	Y	T	N	Y	A	E	N	L	K	T		

CDR3 Comparisons

1G8	1gG _{1k}	G	G	F														
2H9	1gG _{1k}	L	G	R	P	N												
4A10	1gG _{2ak}	R	S	T	M	I	T	T	G	F	A	Y						

FIG. 62

A



B



C



D



FIG. 63

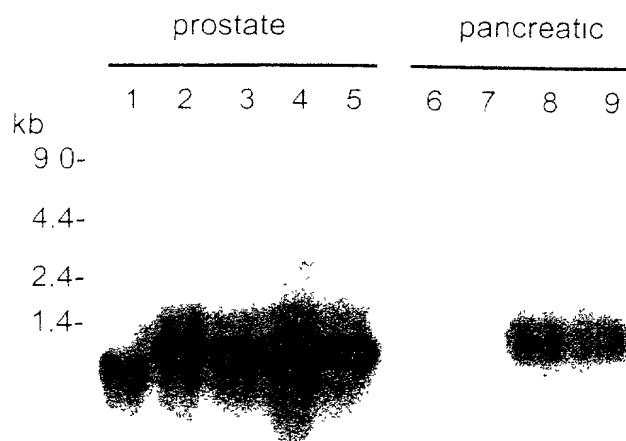


FIG. 64

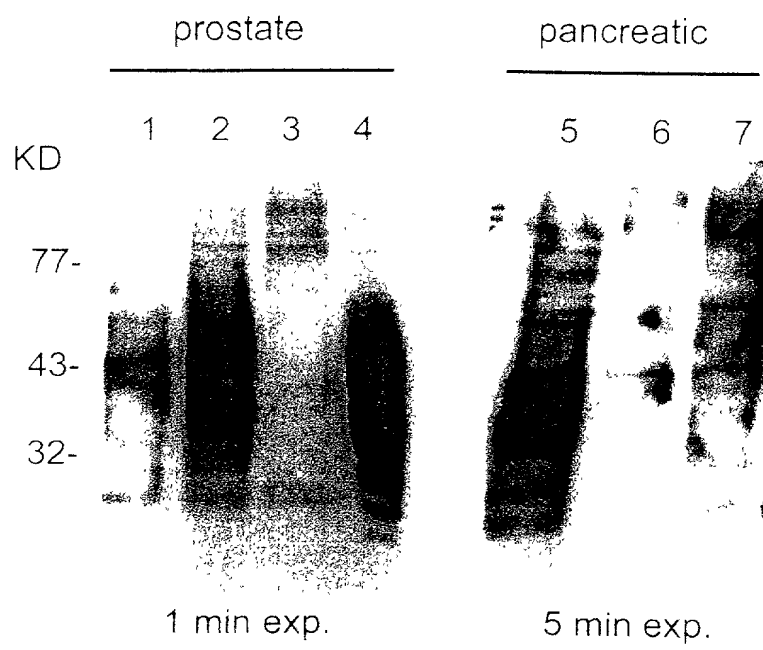


FIG. 65

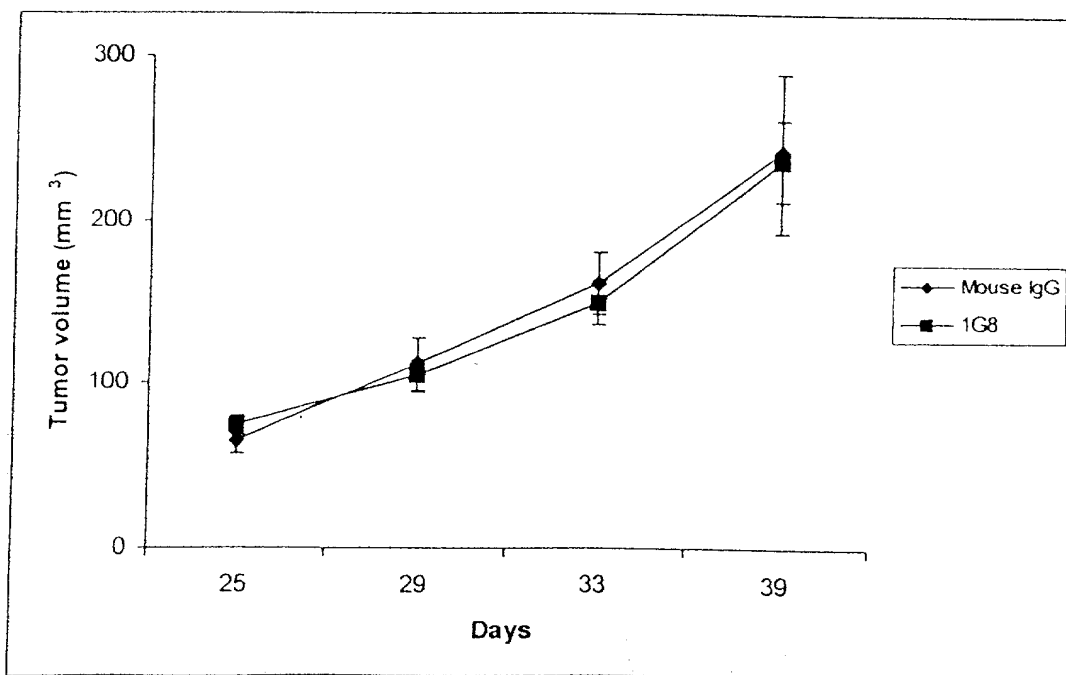
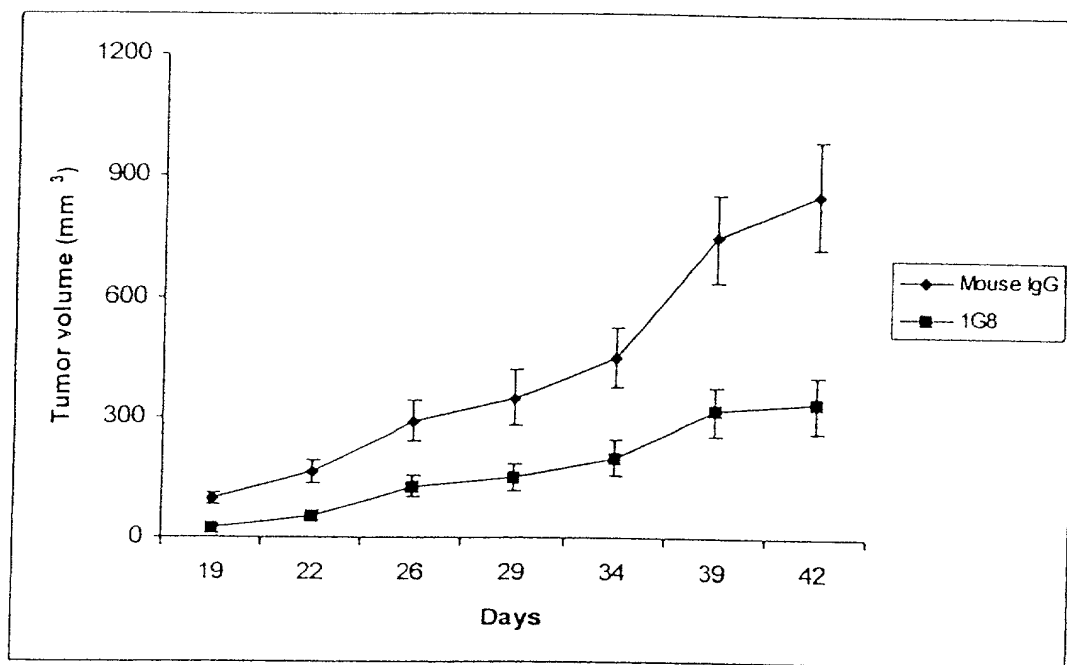
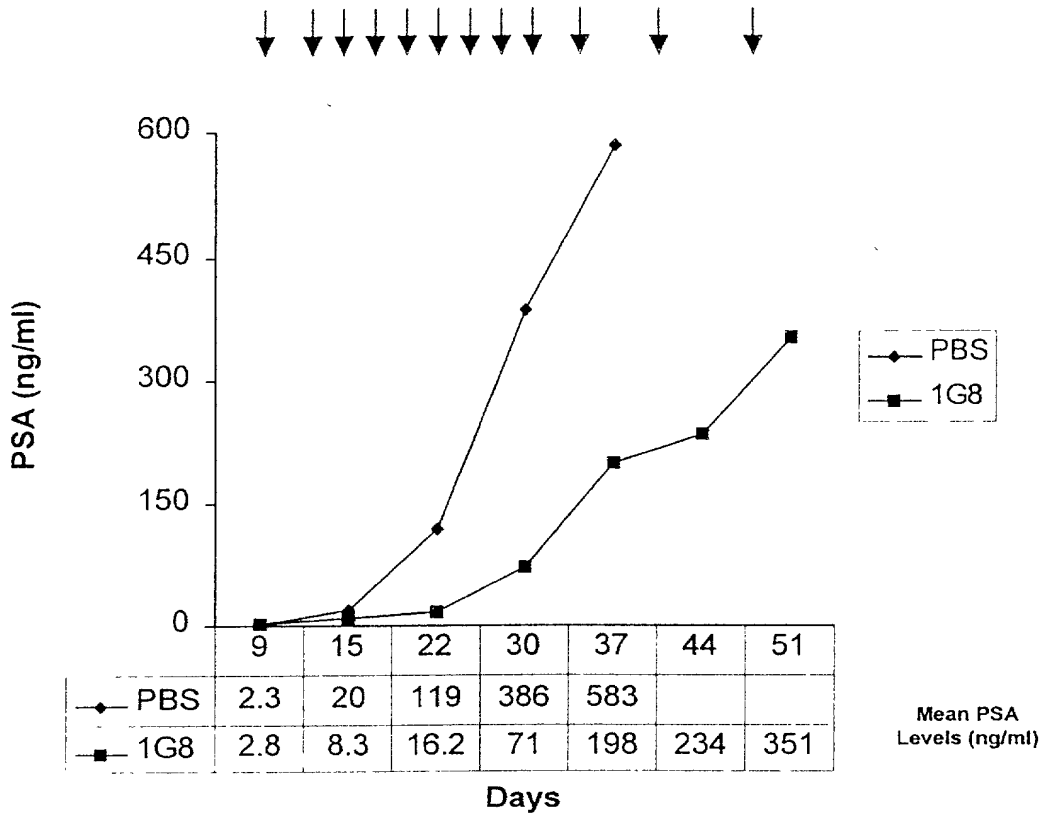


FIG. 66

A)



B)

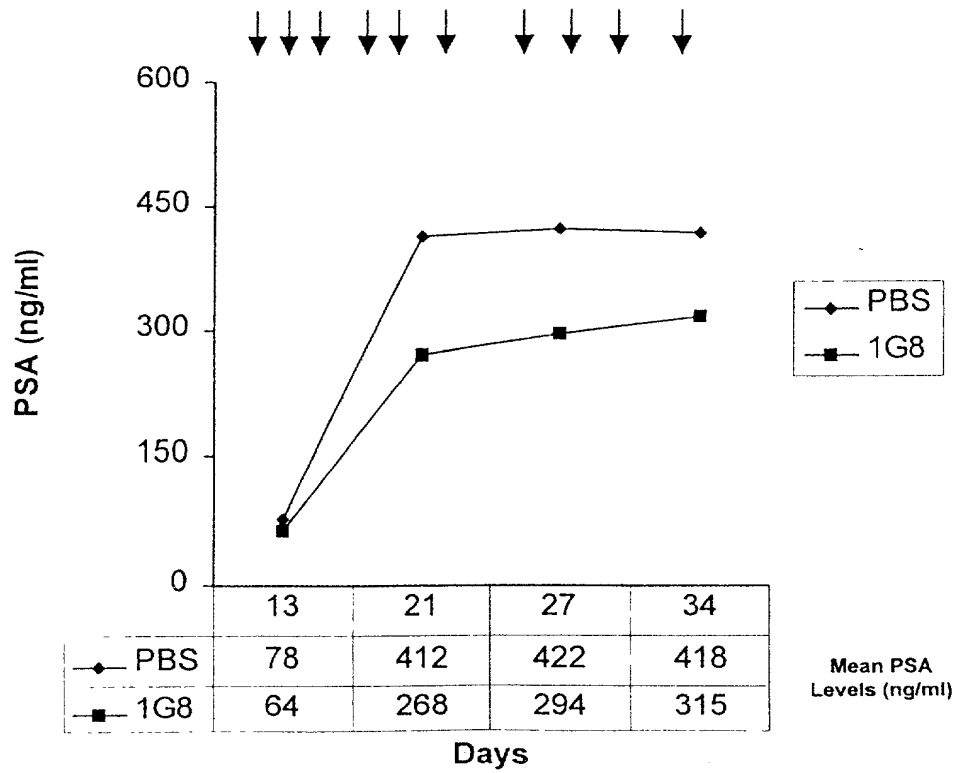
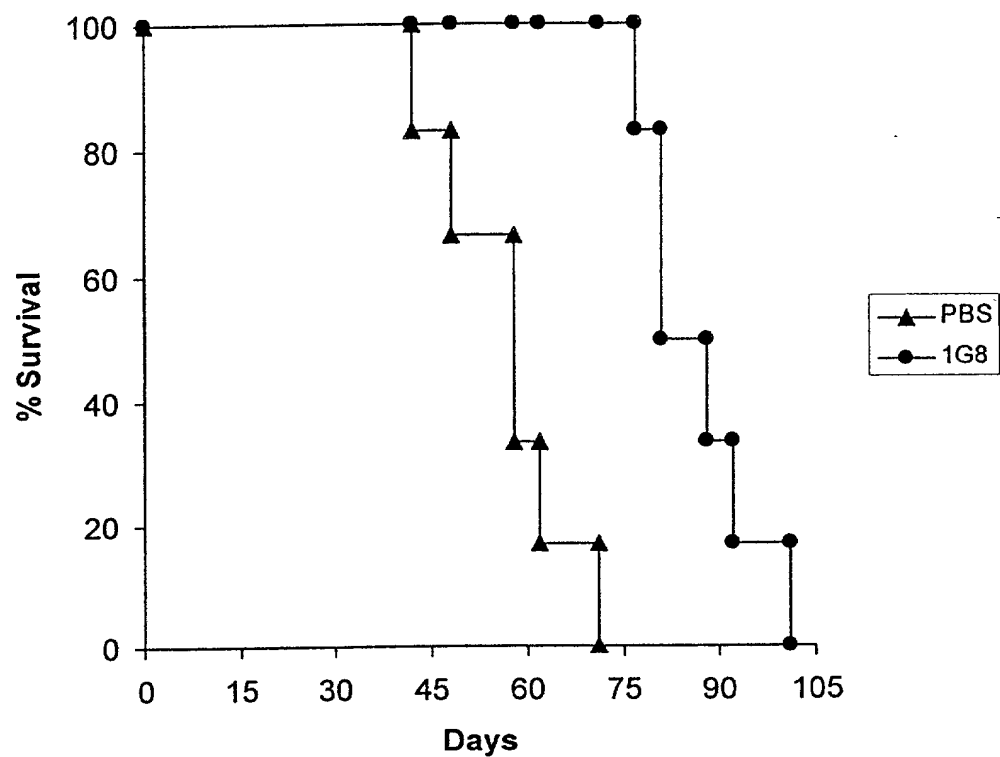


FIG. 67

A)



B)

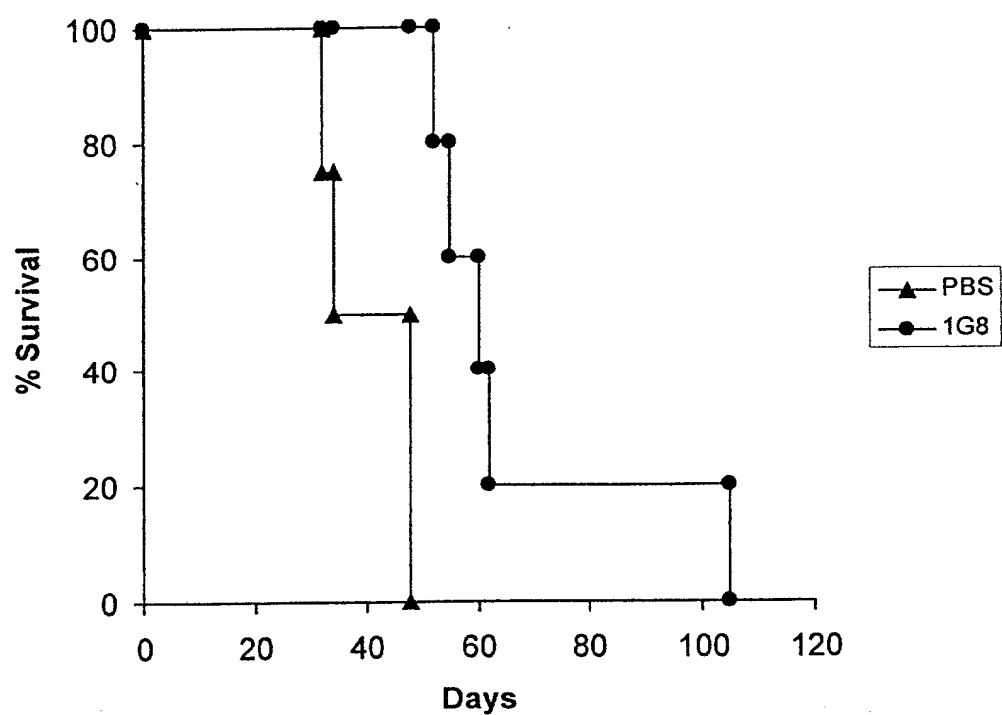
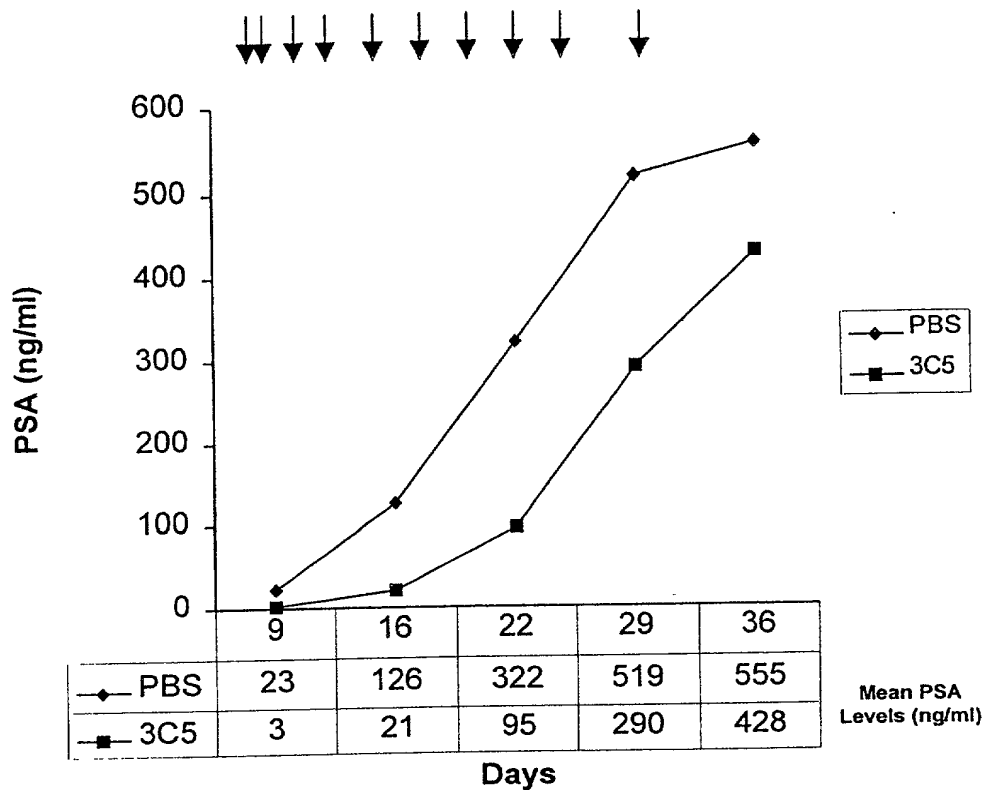


FIG. 68

A)



B)

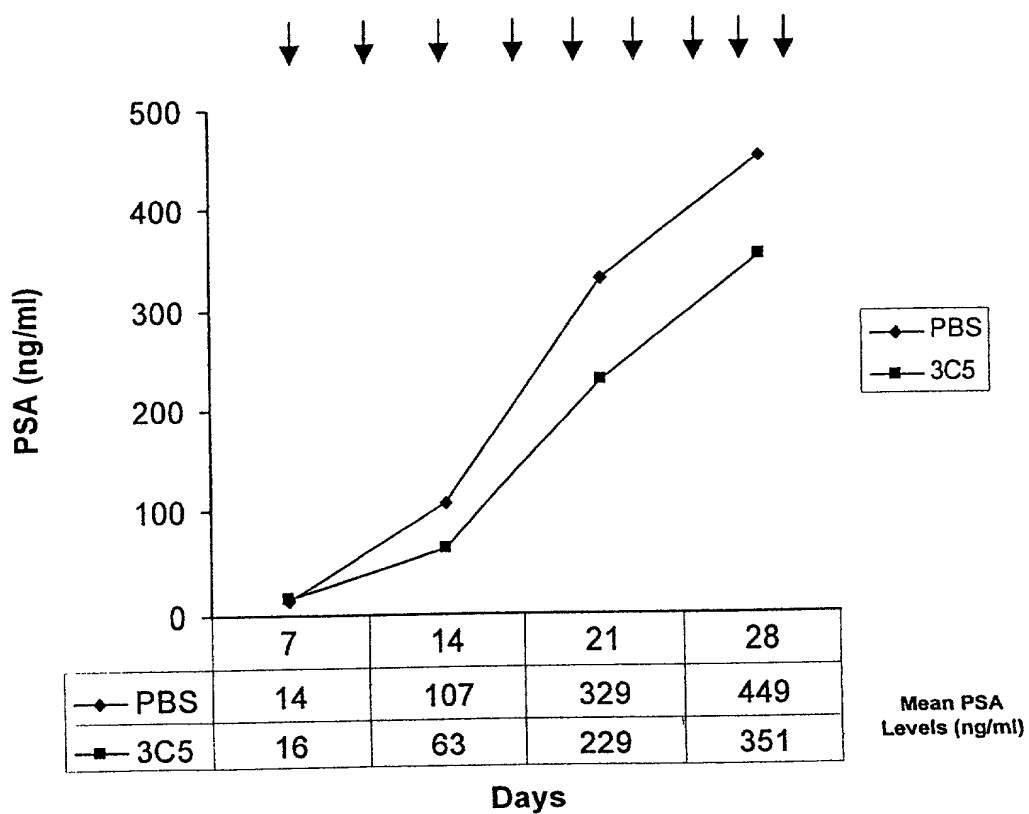
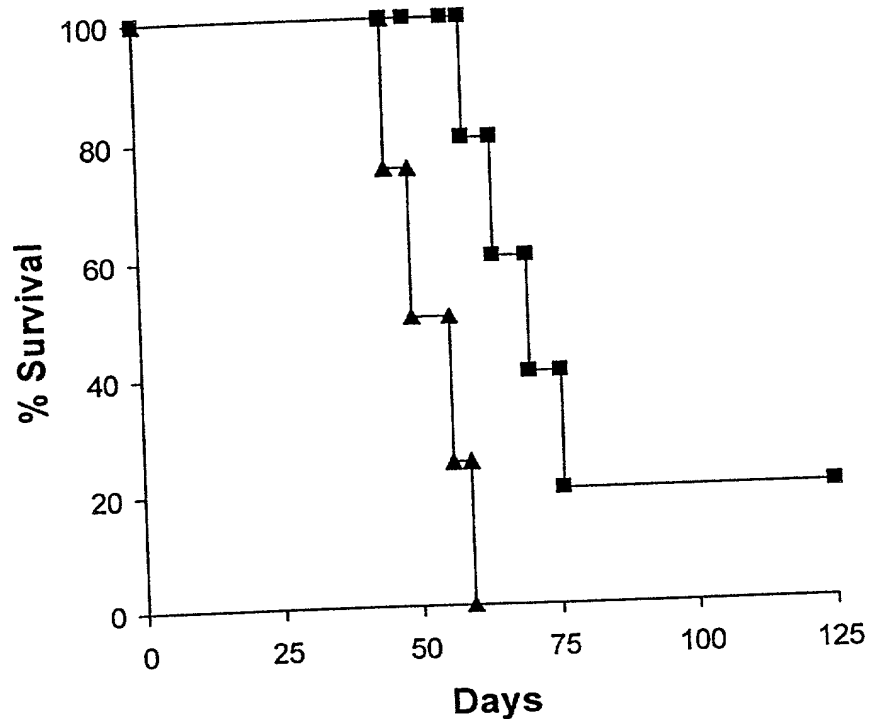


FIG. 69

A)



B)

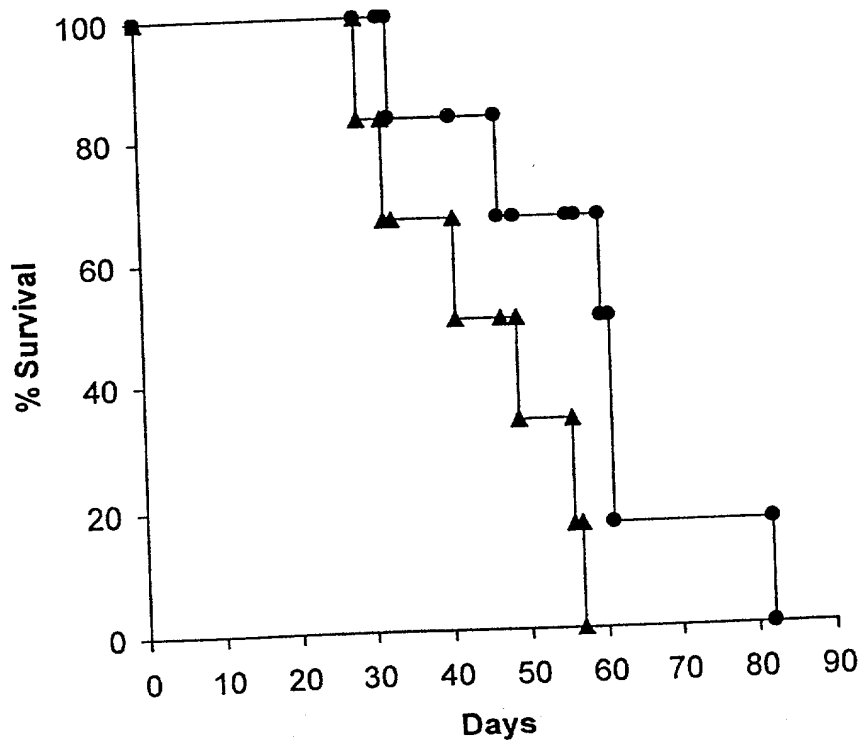


FIG. 70

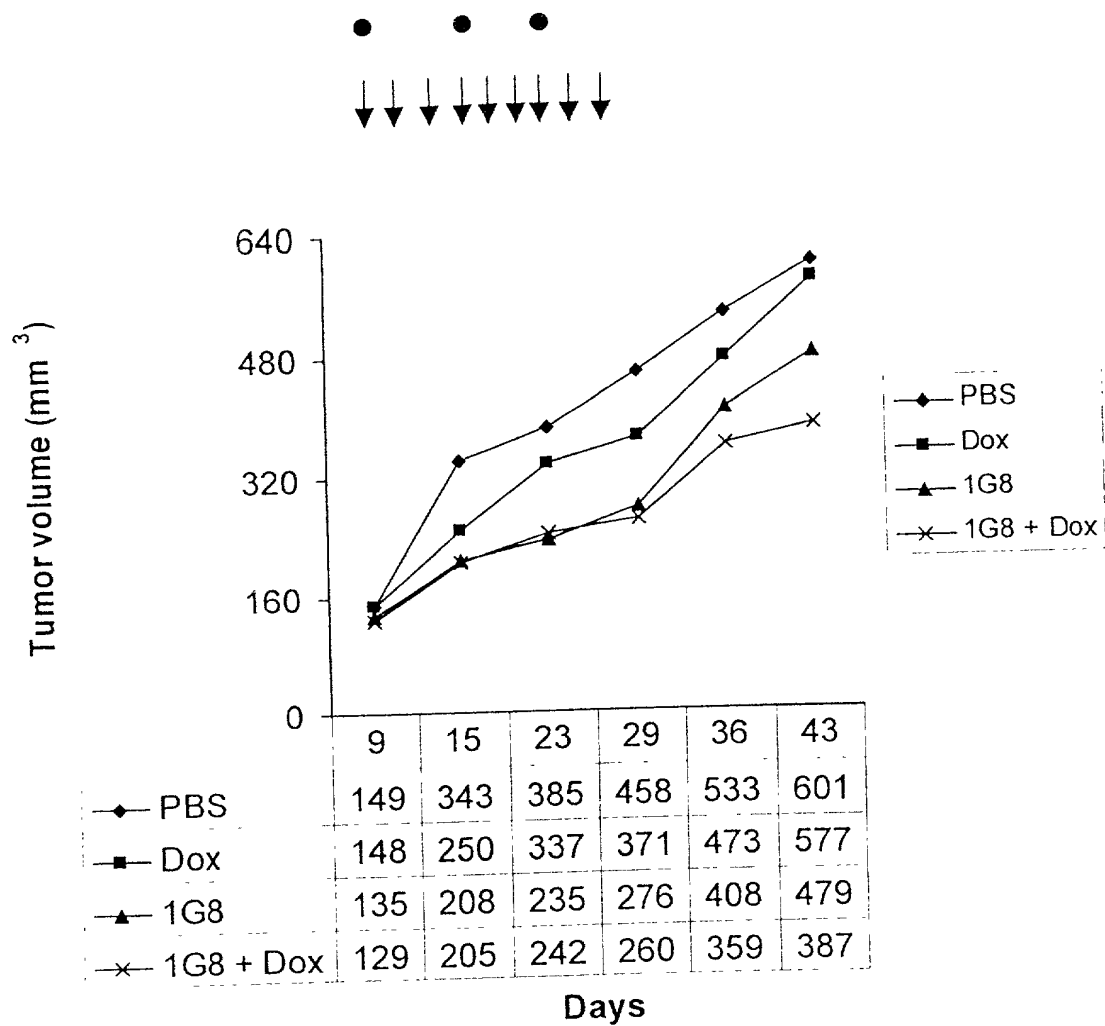
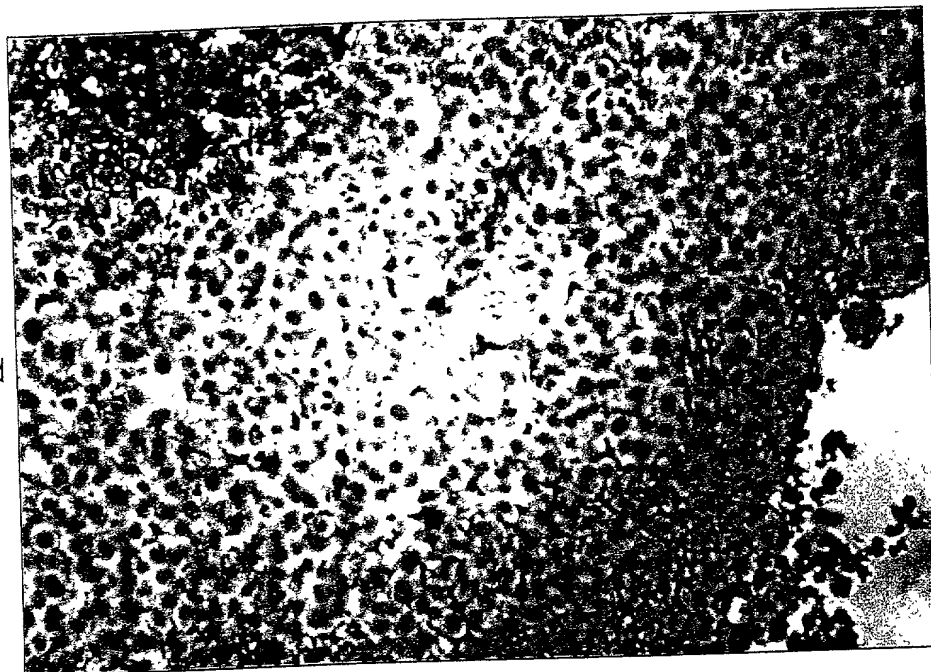
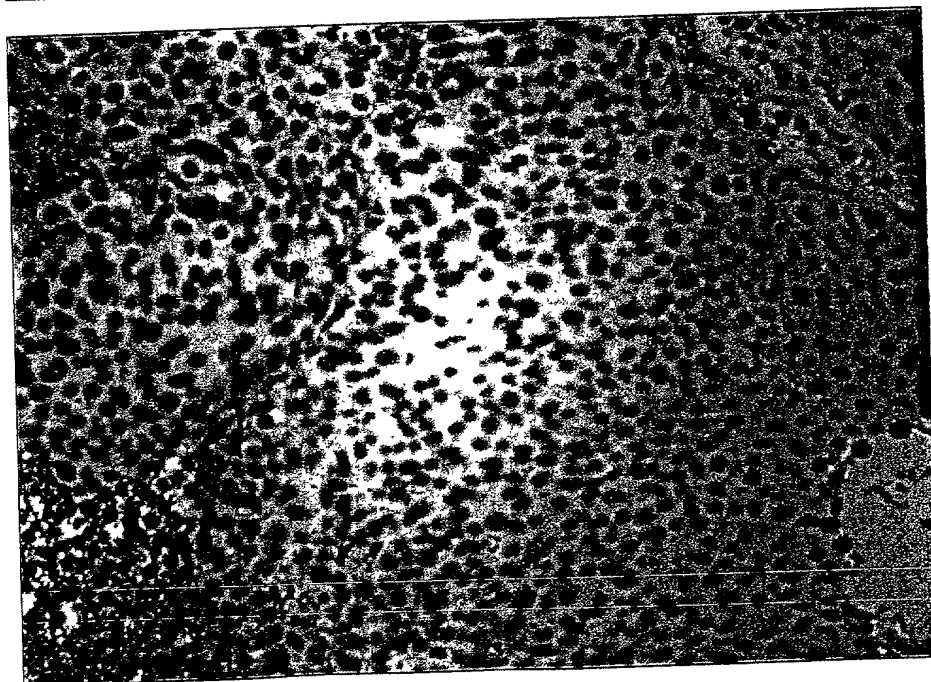


FIG. 71

3C5 Treated



mIgG Treated



006642 073604

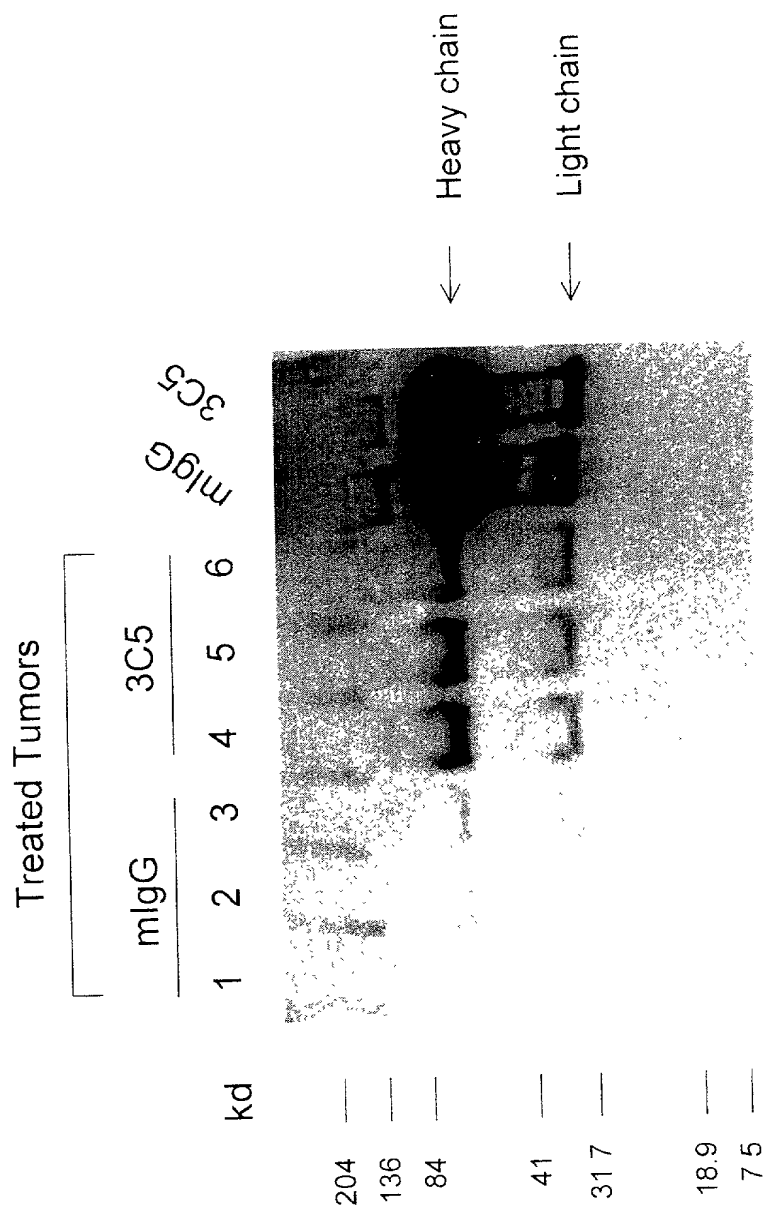


FIG. 72

FIG. 73